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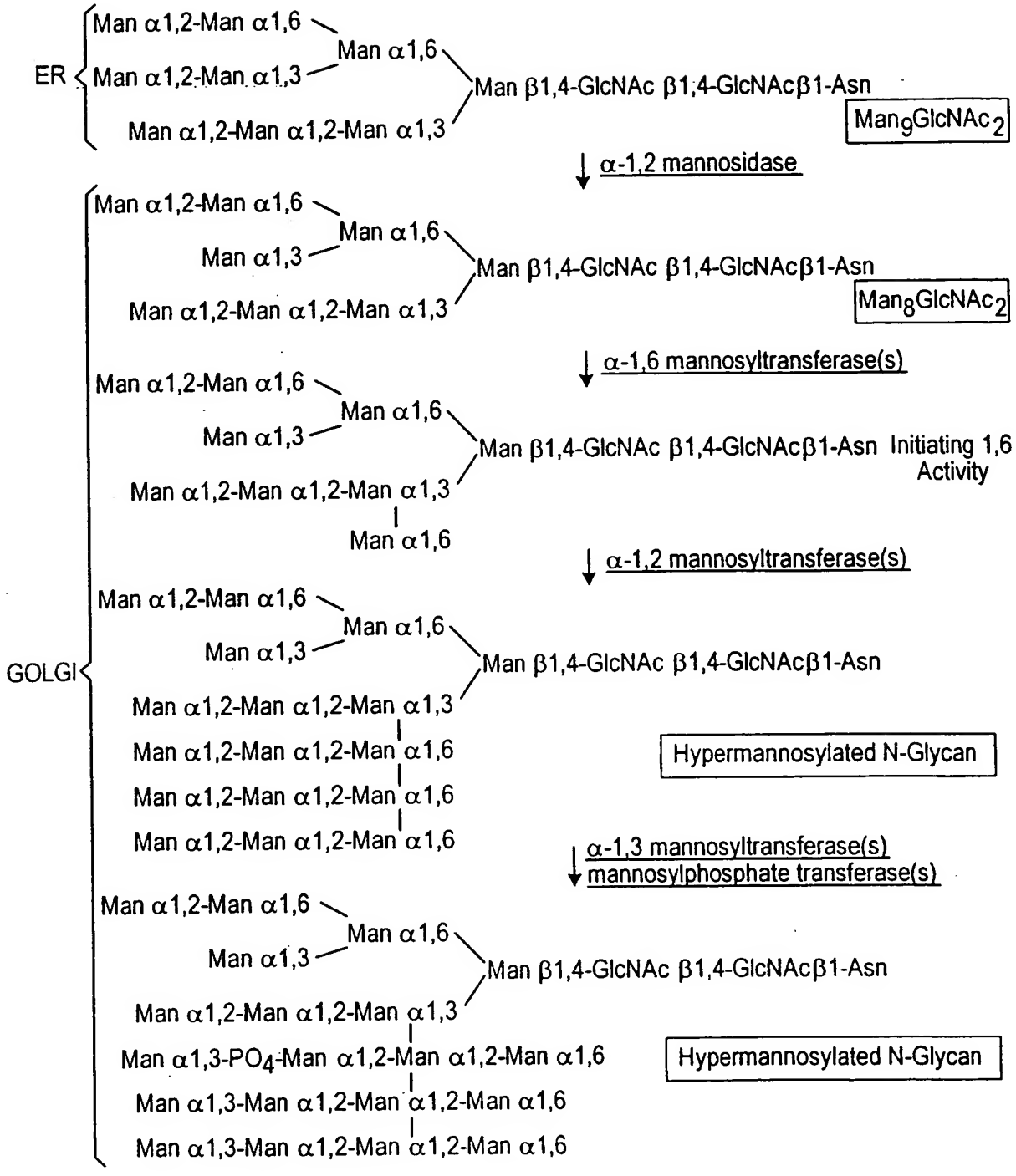


FIG. 1A

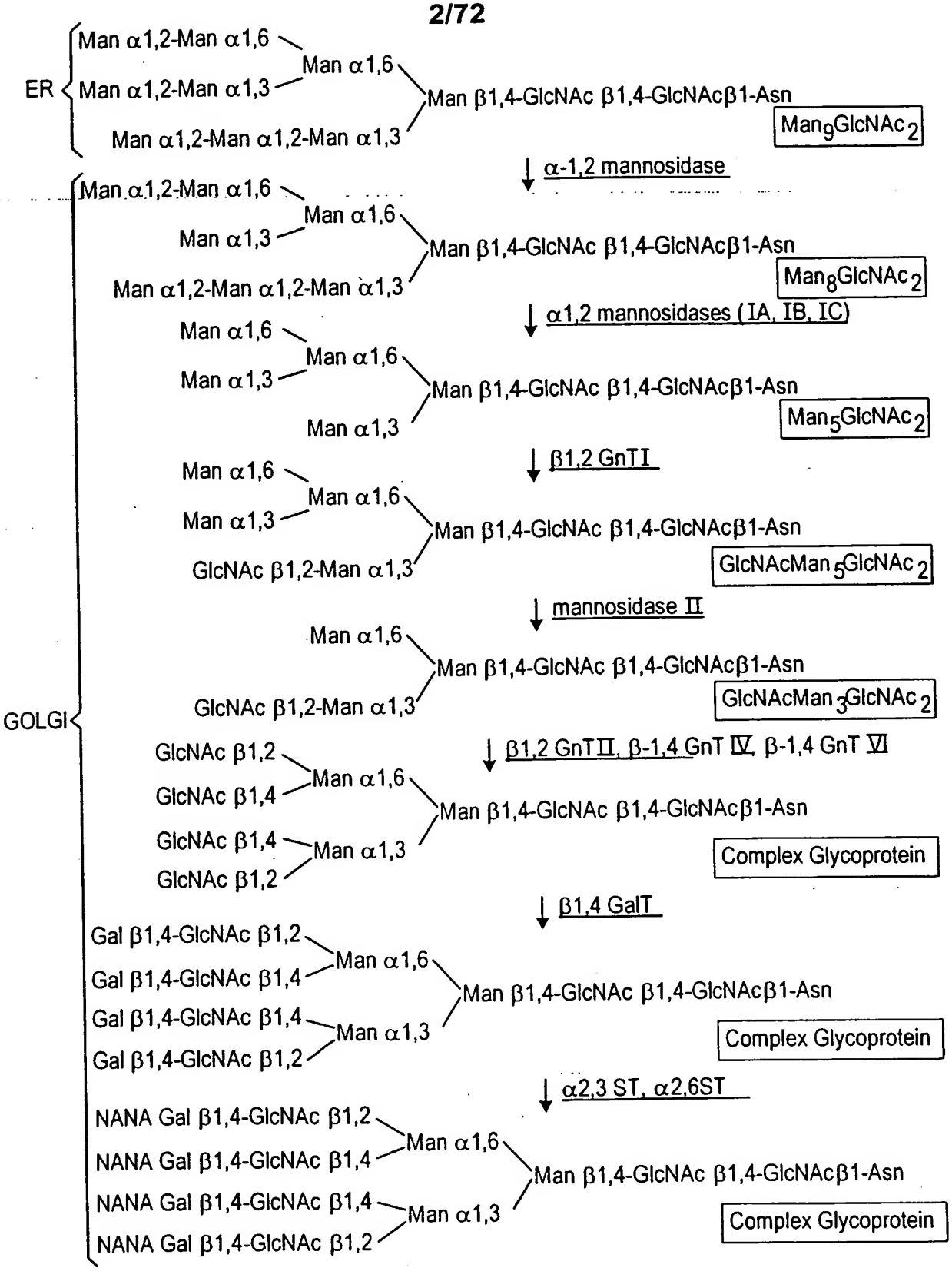

ER
Man α1,2-Man α1,6
Man α1,2-Man α1,3
Man α1,6
Man α1,2-Man α1,2-Man α1,3
Man β1,4-GlcNAc β1,4-GlcNAcβ1-Asn
Man9GlcNAc2
α-1,2 mannosidase
GOLGI
Man α1,2-Man α1,6
Man α1,3
Man α1,6
Man α1,2-Man α1,2-Man α1,3
Man β1,4-GlcNAc β1,4-GlcNAcβ1-Asn
Man8GlcNAc2
α1,2 mannosidases (IA, IB, IC)
Man α1,6
Man α1,3
Man α1,6
Man α1,3
Man β1,4-GlcNAc β1,4-GlcNAcβ1-Asn
Man5GlcNAc2
β1,2 GnTI
Man α1,6
Man α1,3
Man α1,6
GlcNAc β1,2-Man α1,3
Man β1,4-GlcNAc β1,4-GlcNAcβ1-Asn
GlcNAcMan5GlcNAc2
mannosidase II
Man α1,6
GlcNAc β1,2-Man α1,3
Man β1,4-GlcNAc β1,4-GlcNAcβ1-Asn
GlcNAcMan3GlcNAc2
β1,2 GnTII, β-1,4 GnT IV, β-1,4 GnT VI
GlcNAc β1,2
GlcNAc β1,4
Man α1,6
GlcNAc β1,4
GlcNAc β1,2
Man α1,3
Man β1,4-GlcNAc β1,4-GlcNAcβ1-Asn
Complex Glycoprotein
β1,4 GalT
Gal β1,4-GlcNAc β1,2
Gal β1,4-GlcNAc β1,4
Man α1,6
Gal β1,4-GlcNAc β1,4
Gal β1,4-GlcNAc β1,2
Man α1,3
Man β1,4-GlcNAc β1,4-GlcNAcβ1-Asn
Complex Glycoprotein
α2,3 ST, α2,6ST
NANA Gal β1,4-GlcNAc β1,2
NANA Gal β1,4-GlcNAc β1,4
Man α1,6
NANA Gal β1,4-GlcNAc β1,4
NANA Gal β1,4-GlcNAc β1,2
Man α1,3
Man β1,4-GlcNAc β1,4-GlcNAcβ1-Asn
Complex Glycoprotein

FIG. 1B

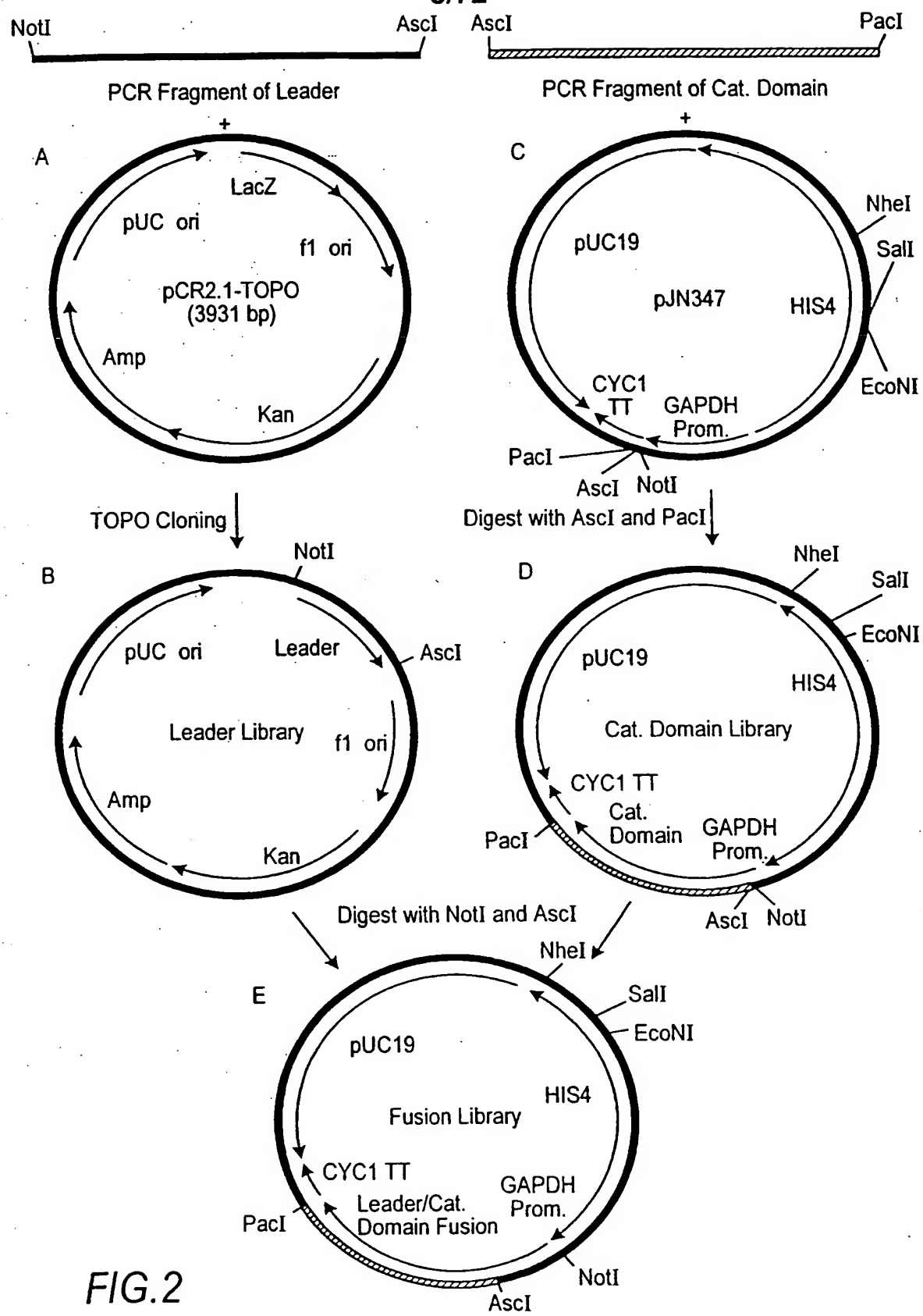

NotI
AscI
AscI
PacI
PCR Fragment of Leader
PCR Fragment of Cat. Domain
A
LacZ
pUC ori
f1 ori
pCR2.1-TOPO
(3931 bp)
Amp
Kan
C
NheI
pUC19
SalI
pJN347
HIS4
EcoNI
CYC1
TT
GAPDH
Prom.
PacI
AscI
NotI
TOPO Cloning
Digest with AscI and PacI
B
NotI
pUC ori
Leader
AscI
Leader Library
f1 ori
Amp
Kan
D
NheI
SalI
EcoNI
pUC19
HIS4
Cat. Domain Library
CYC1 TT
Cat.
Domain
GAPDH
Prom.
PacI
AscI
NotI
Digest with NotI and AscI
E
NheI
SalI
EcoNI
pUC19
HIS4
Fusion Library
CYC1 TT
GAPDH
Prom.
Leader/Cat.
Domain Fusion
PacI
NotI
AscI

FIG.2

M. musculus alpha-1,2-mannosidase IA open reading frame. The transmembrane and catalytic domains are highlighted in bold respectively. The sequence of the primers used to generate the N-terminal truncations are highlighted by underlining and the start of each respective protein fragment indicated by an arrow.

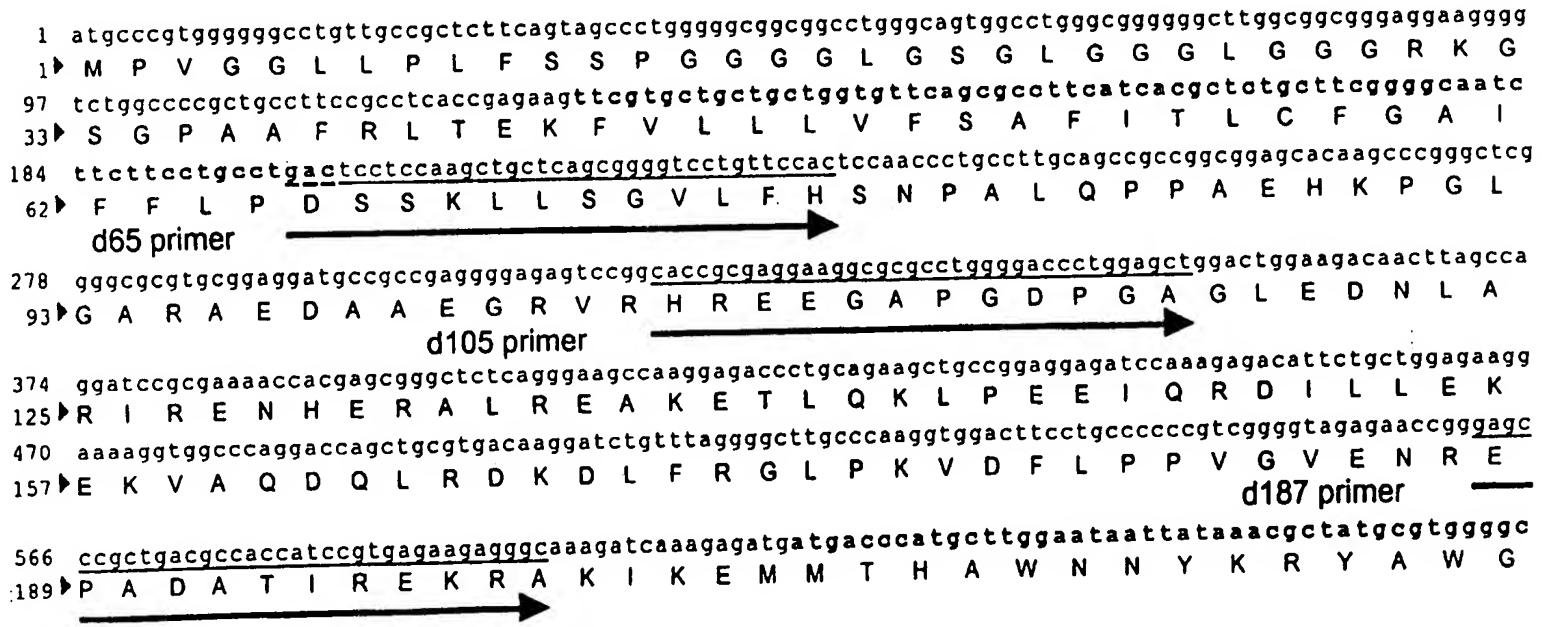


FIG. 3

```
655 ttgaacgaactgaaacctatatcaaaagaaggccattcaagcagtttgtttggcaacatcaaaggagctacaatagtagatg
219▶ L  N  E  L  K  P  I  S  K  E  G  H  S  S  S  L  F  G  N  I  K  G  A  T  I  V  D
737 ccctggataccctttttcattatgggcatgaagactgaatttcaagaagctaaatcgtggattaaaaaatatttagattttaa
246▶A  L  D  T  L  F  I  M  G  M  K  T  E  F  Q  E  A  K  S  W  I  K  K  Y  L  D  F  N
819 tgtgaatgctgaagtttctgtttttgaagtcaacatacgcttcgtcggtggactgctgtcagcctactatttgtccggagag
273▶  V  N  A  E  V  S  V  F  E  V  N  I  R  F  V  G  G  L  L  S  A  Y  Y  L  S  G  E
901 gagatatttcgaaagaaagcagtggaacttggggtaaaattgctacctgcatttcatactccctctggaatacctgggcat
301▶ E  I  F  R  K  K  A  V  E  L  G  V  K  L  L  P  A  F  H  T  P  S  G  I  P  W  A
983 tgctgaatatgaaaagtgggatcgggcggaactggccctgggcctctggaggcagcagtatcctggccgaatttggaactct
328▶L  L  N  M  K  S  G  I  G  R  N  W  P  W  A  S  G  G  S  S  I  L  A  E  F  G  T  L
1065 gcatttagagtttatgcacttgtcccacttatcaggagacccagtctttgccgaaaaggttatgaaaattcgaacagtgttg
355▶  H  L  E  F  M  H  L  S  H  L  S  G  D  P  V  F  A  E  K  V  M  K  I  R  T  V  L
1147 aacaaactggacaaaccagaaggcctttatcctaactatctgaaccccagtagtggacagtggggtcaacatcatgtgtcgg
383▶ N  K  L  D  K  P  E  G  L  Y  P  N  Y  L  N  P  S  S  G  Q  W  G  Q  H  H  V  S
1229 ttggaggacttggagacagcttttatgaatatttgcttaaggcgtggttaatgtctgacaagacagatctcgaagccaagaa
410▶V  G  G  L  G  D  S  F  Y  E  Y  L  L  K  A  W  L  M  S  D  K  T  D  L  E  A  K  K
1311 gatgtattttgatgctgttcaggccatcgagactcacttgatccgcaagtcaagtgggggactaacgtacatcgcagagtgg
437▶  M  Y  F  D  A  V  Q  A  I  E  T  H  L  I  R  K  S  S  G  G  L  T  Y  I  A  E  W
1393 aaggggggcctcctggaacacaagatgggccacctgacgtgctttgcaggaggcatgtttgcacttggggcagatggagctc
465▶ K  G  G  L  L  E  H  K  M  G  H  L  T  C  F  A  G  G  M  F  A  L  G  A  D  G  A
1475 cggaagcccgggcccaacactaccttgaactcggagctgaaattgcccgcacttgtcatgaatcttataatcgtacatatgt
492▶P  E  A  R  A  Q  H  Y  L  E  L  G  A  E  I  A  R  T  C  H  E  S  Y  N  R  T  Y  V
1557 gaagttgggaccggaagcgtttcgatttgatggcggtgtggaagctattgccacgaggcaaaatgaaaagtattacatcttta
519▶  K  L  G  P  E  A  F  R  F  D  G  G  V  E  A  I  A  T  R  Q  N  E  K  Y  Y  I  L
1639 cggcccgaggtcatcgagacatacatgtacatgtggcgactgactcacgaccccaagtacaggacctgggcctgggaagccg
547▶ R  P  E  V  I  E  T  Y  M  Y  M  W  R  L  T  H  D  P  K  Y  R  T  W  A  W  E  A
1721 tggaggctctagaaagtcactgcagagtgaacggaggctactcaggcttacgggatgtttacattgcccgtgagagttatga
574▶V  E  A  L  E  S  H  C  R  V  N  G  G  Y  S  G  L  R  D  V  Y  I  A  R  E  S  Y  D
1803 cgatgtccagcaaagtttcttcctggcagagacactgaagtatttgtacttgatattttccgatgatgaccttcttccacta
601▶  D  V  Q  Q  S  F  F  L  A  E  T  L  K  Y  L  Y  L  I  F  S  D  D  D  L  L  P  L
1885 gaacactggatcttcaacaccgaggctcatcctttccctatactccgtgaacagaagaaggaaattgatggcaaagagaaatga
629▶ E  H  W  I  F  N  T  E  A  H  P  F  P  I  L  R  E  Q  K  K  E  I  D  G  K  E  K
```

FIG. 3 CON'T

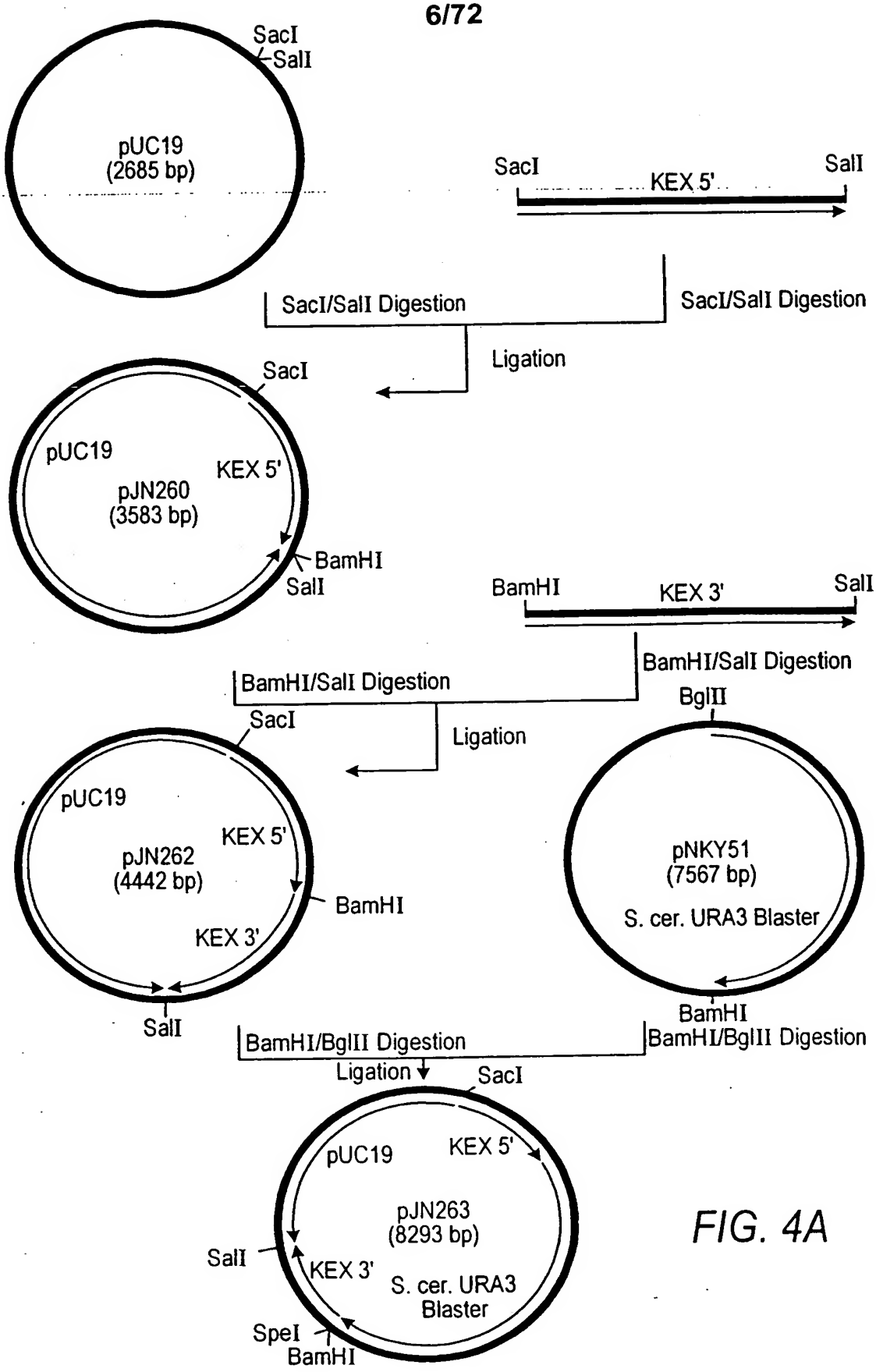

SacI
SalI
pUC19
(2685 bp)
SacI
KEX 5'
SalI
SacI/SalI Digestion
SacI/SalI Digestion
Ligation
SacI
pUC19
KEX 5'
pJN260
(3583 bp)
BamHI
SalI
BamHI
KEX 3'
SalI
BamHI/SalI Digestion
BamHI/SalI Digestion
BglII
SacI
Ligation
pUC19
KEX 5'
pJN262
(4442 bp)
BamHI
KEX 3'
SalI
pNKY51
(7567 bp)
S. cer. URA3 Blaster
BamHI
BamHI/BglII Digestion
BamHI/BglII Digestion
Ligation
SacI
pUC19
KEX 5'
pJN263
(8293 bp)
SalI
KEX 3'
S. cer. URA3
Blaster
SpeI
BamHI

FIG. 4A

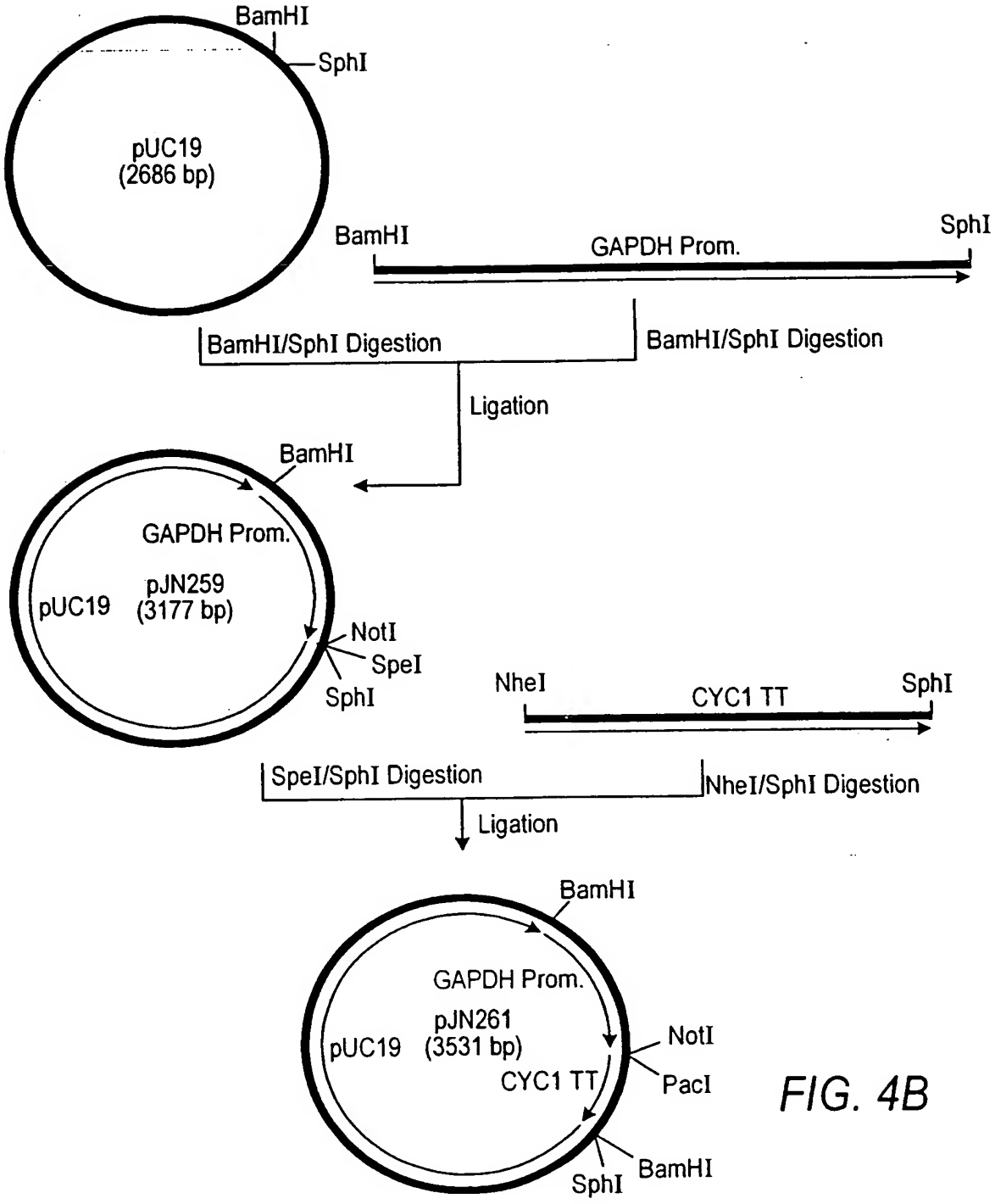

BamHI
SphI
pUC19
(2686 bp)
BamHI
GAPDH Prom.
SphI
BamHI/SphI Digestion
BamHI/SphI Digestion
Ligation
BamHI
GAPDH Prom.
pJN259
pUC19
(3177 bp)
NotI
SpeI
SphI
NheI
CYC1 TT
SphI
SpeI/SphI Digestion
NheI/SphI Digestion
Ligation
BamHI
GAPDH Prom.
pJN261
pUC19
(3531 bp)
CYC1 TT
NotI
PacI
SphI
BamHI

FIG. 4B

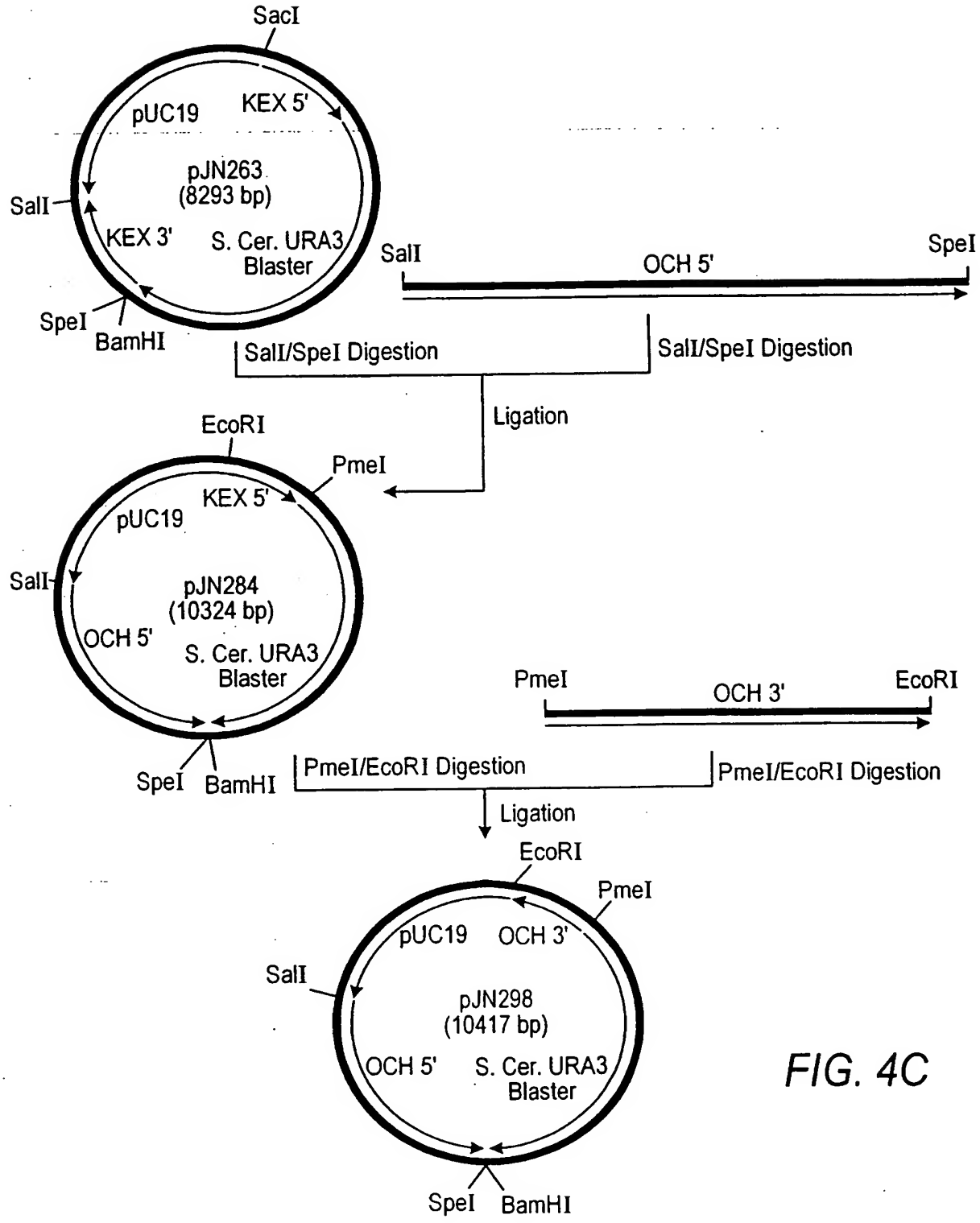

SacI
pUC19
KEX 5'
pJN263
(8293 bp)
SalI
KEX 3'
S. Cer. URA3
Blaster
SpeI
BamHI
SalI
OCH 5'
SpeI
SalI/SpeI Digestion
SalI/SpeI Digestion
Ligation
EcoRI
PmeI
KEX 5'
pUC19
SalI
pJN284
(10324 bp)
OCH 5'
S. Cer. URA3
Blaster
SpeI
BamHI
PmeI
OCH 3'
EcoRI
PmeI/EcoRI Digestion
PmeI/EcoRI Digestion
Ligation
EcoRI
PmeI
pUC19
OCH 3'
SalI
pJN298
(10417 bp)
OCH 5'
S. Cer. URA3
Blaster
SpeI
BamHI

FIG. 4C

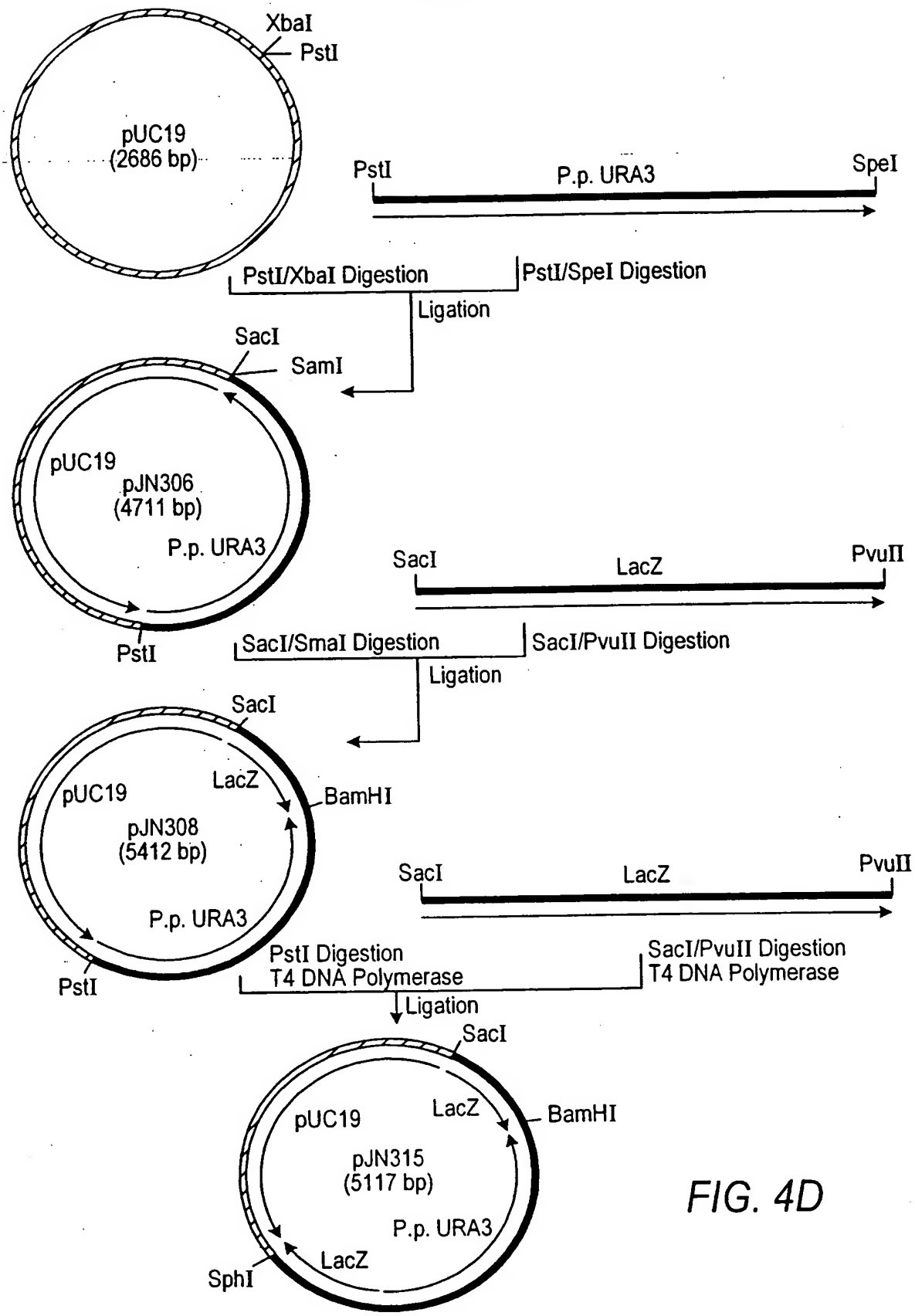

XbaI
PstI
pUC19
(2686 bp)
PstI
P.p. URA3
SpeI
PstI/XbaI Digestion
PstI/SpeI Digestion
Ligation
SacI
SamI
pUC19
pJN306
(4711 bp)
P.p. URA3
PstI
SacI
LacZ
PvuII
SacI/SmaI Digestion
SacI/PvuII Digestion
Ligation
SacI
pUC19
LacZ
BamHI
pJN308
(5412 bp)
P.p. URA3
PstI
SacI
LacZ
PvuII
PstI Digestion
T4 DNA Polymerase
SacI/PvuII Digestion
T4 DNA Polymerase
Ligation
SacI
pUC19
LacZ
BamHI
pJN315
(5117 bp)
P.p. URA3
LacZ
SphI

FIG. 4D

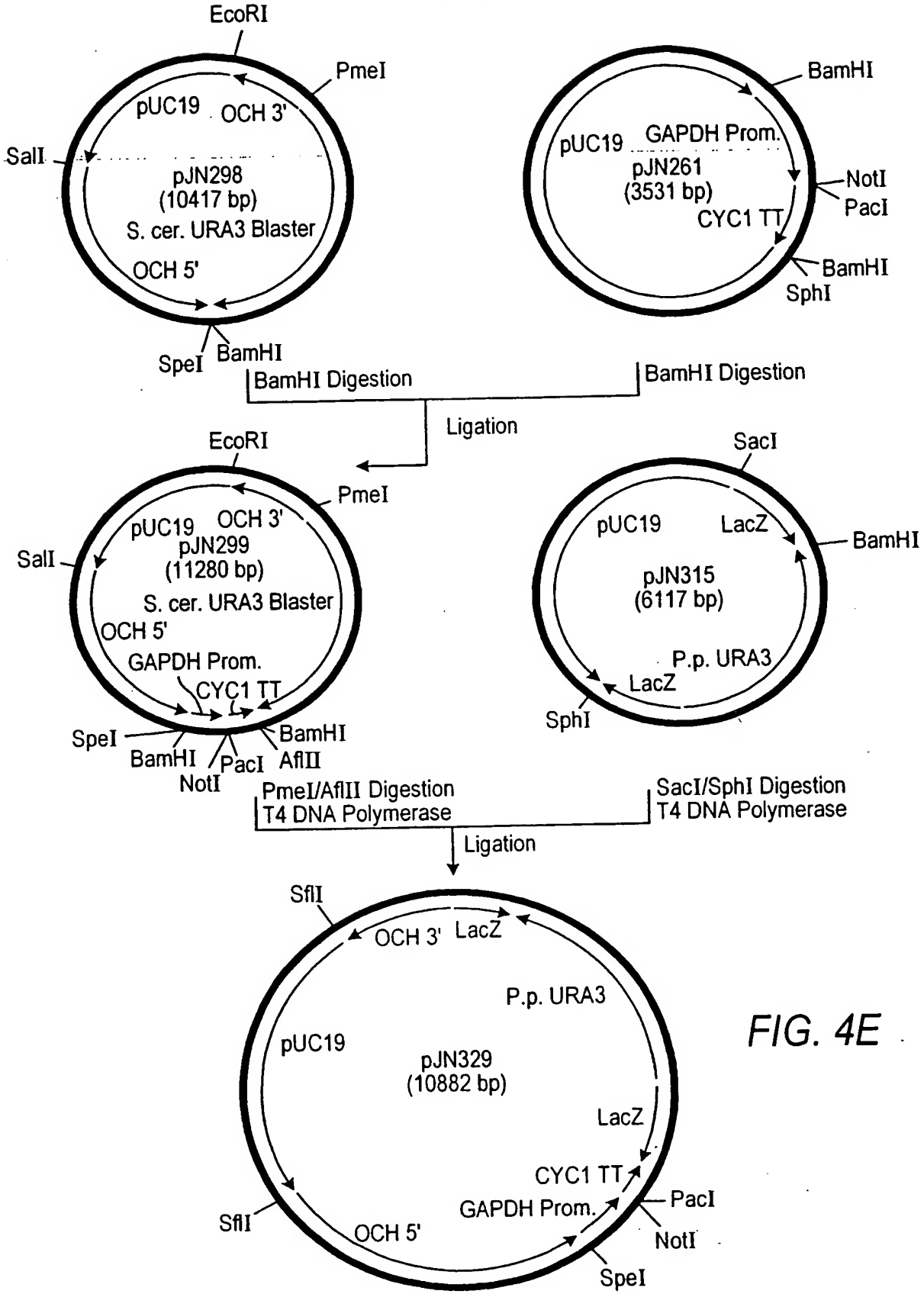

EcoRI
PmeI
pUC19
OCH 3'
SalI
pJN298
(10417 bp)
S. cer. URA3 Blaster
OCH 5'
SpeI
BamHI
BamHI
pUC19
GAPDH Prom.
pJN261
(3531 bp)
CYC1 TT
NotI
PacI
BamHI
SphI
BamHI Digestion
BamHI Digestion
Ligation
EcoRI
PmeI
SalI
pUC19
OCH 3'
pJN299
(11280 bp)
S. cer. URA3 Blaster
OCH 5'
GAPDH Prom.
CYC1 TT
SpeI
BamHI
BamHI
PacI
AflII
NotI
SacI
pUC19
LacZ
BamHI
pJN315
(6117 bp)
P.p. URA3
LacZ
SphI
PmeI/AflII Digestion
T4 DNA Polymerase
SacI/SphI Digestion
T4 DNA Polymerase
Ligation
SfiI
OCH 3'
LacZ
P.p. URA3
pUC19
pJN329
(10882 bp)
LacZ
CYC1 TT
GAPDH Prom.
PacI
NotI
SfiI
OCH 5'
SpeI

FIG. 4E

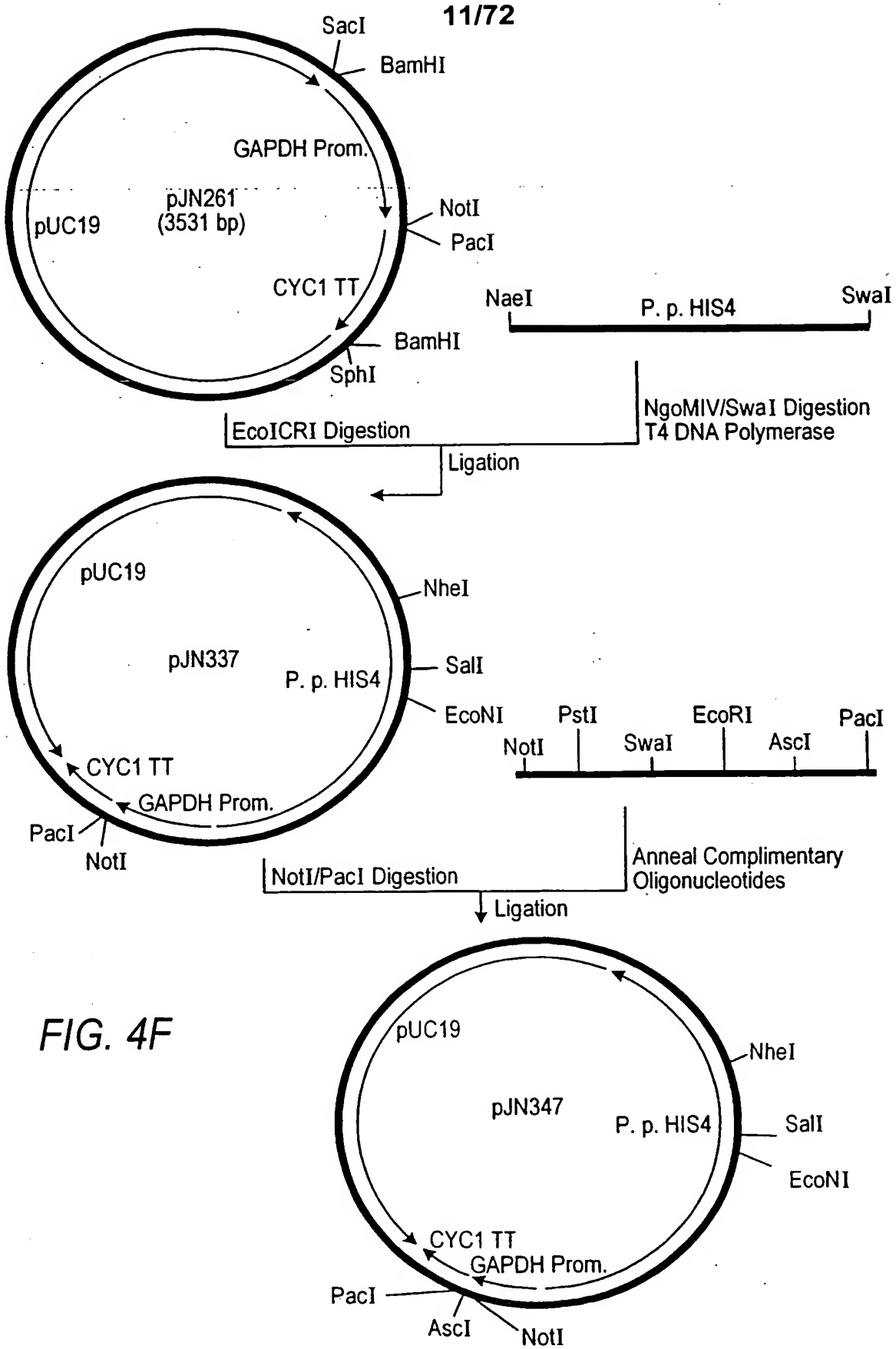

SacI
BamHI
GAPDH Prom.
pJN261
(3531 bp)
pUC19
NotI
PacI
CYC1 TT
BamHI
SphI
NaeI
P. p. HIS4
SwaI
NgoMIV/SwaI Digestion
T4 DNA Polymerase
EcoICRI Digestion
Ligation
pUC19
NheI
pJN337
SalI
P. p. HIS4
EcoNI
PstI
EcoRI
PacI
NotI
SwaI
AscI
CYC1 TT
GAPDH Prom.
PacI
NotI
Anneal Complimentary
Oligonucleotides
NotI/PacI Digestion
Ligation
pUC19
NheI
pJN347
SalI
P. p. HIS4
EcoNI
CYC1 TT
GAPDH Prom.
PacI
AscI
NotI

FIG. 4F

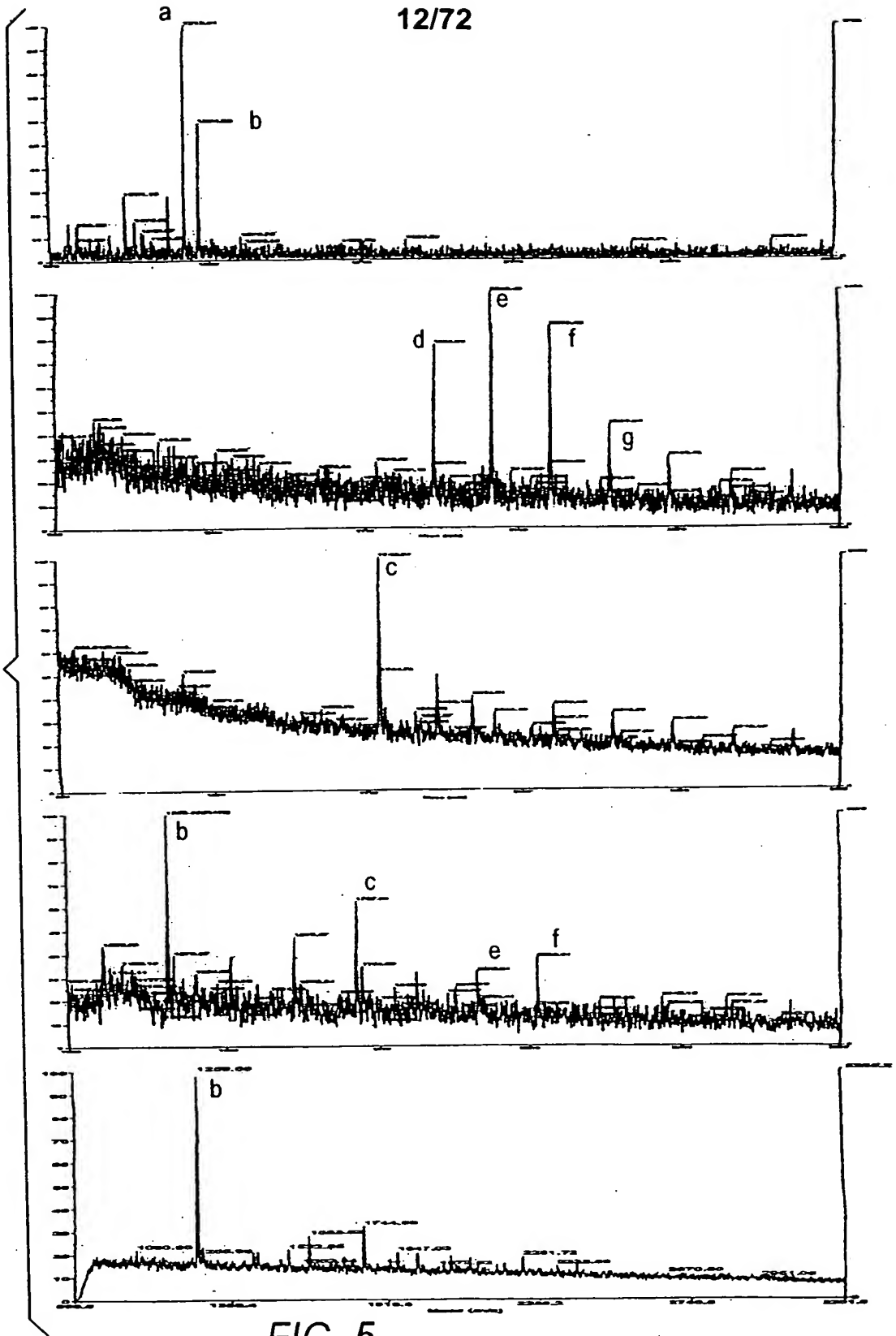


FIG. 5

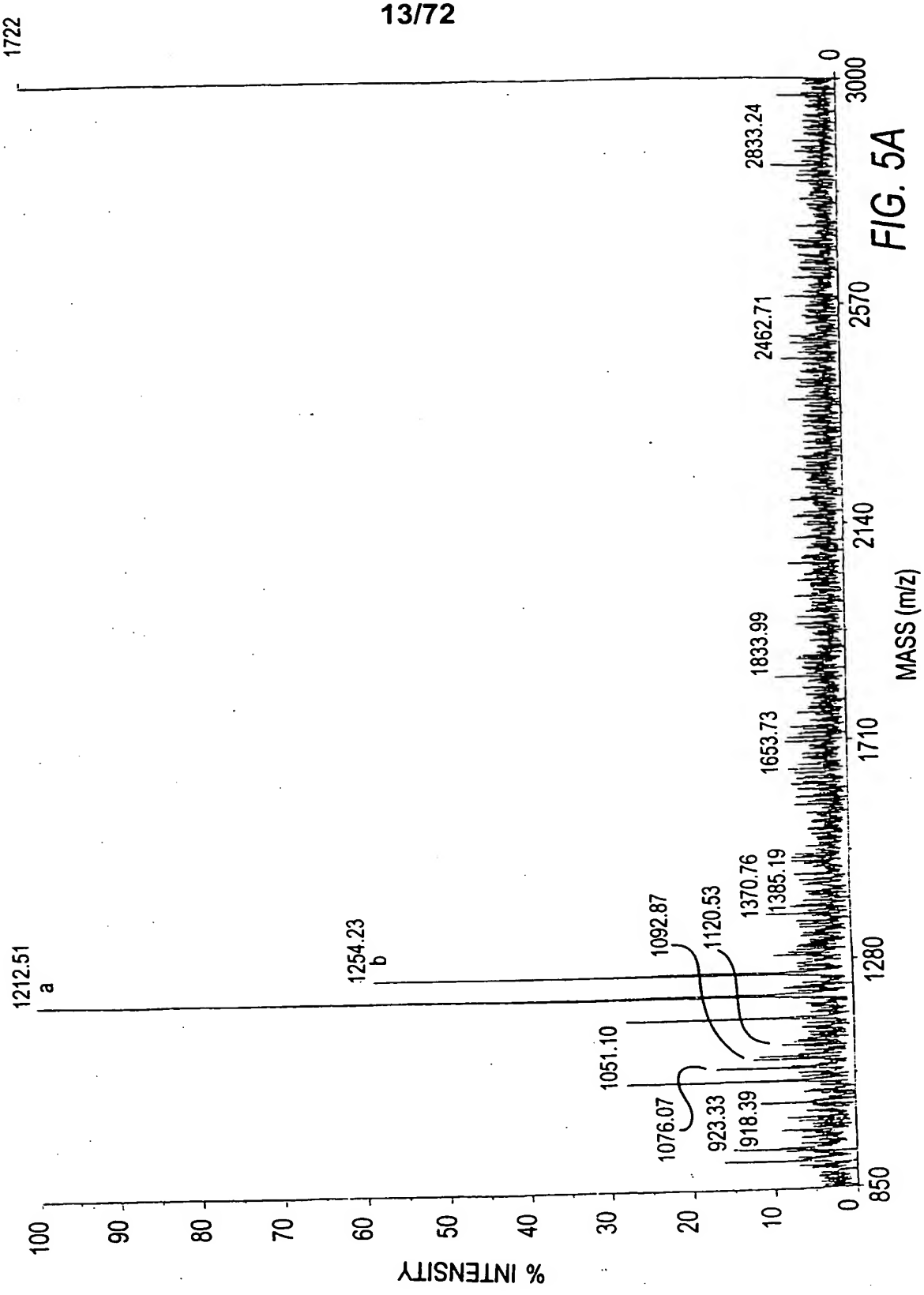

% INTENSITY
MASS (m/z)
100
90
80
70
60
50
40
30
20
10
0
850
1280
1710
2140
2570
3000
1212.51
a
1254.23
b
1092.87
1120.53
1370.76
1385.19
1653.73
1833.99
2462.71
2833.24
1722
1051.10
1076.07
923.33
918.39

FIG. 5A

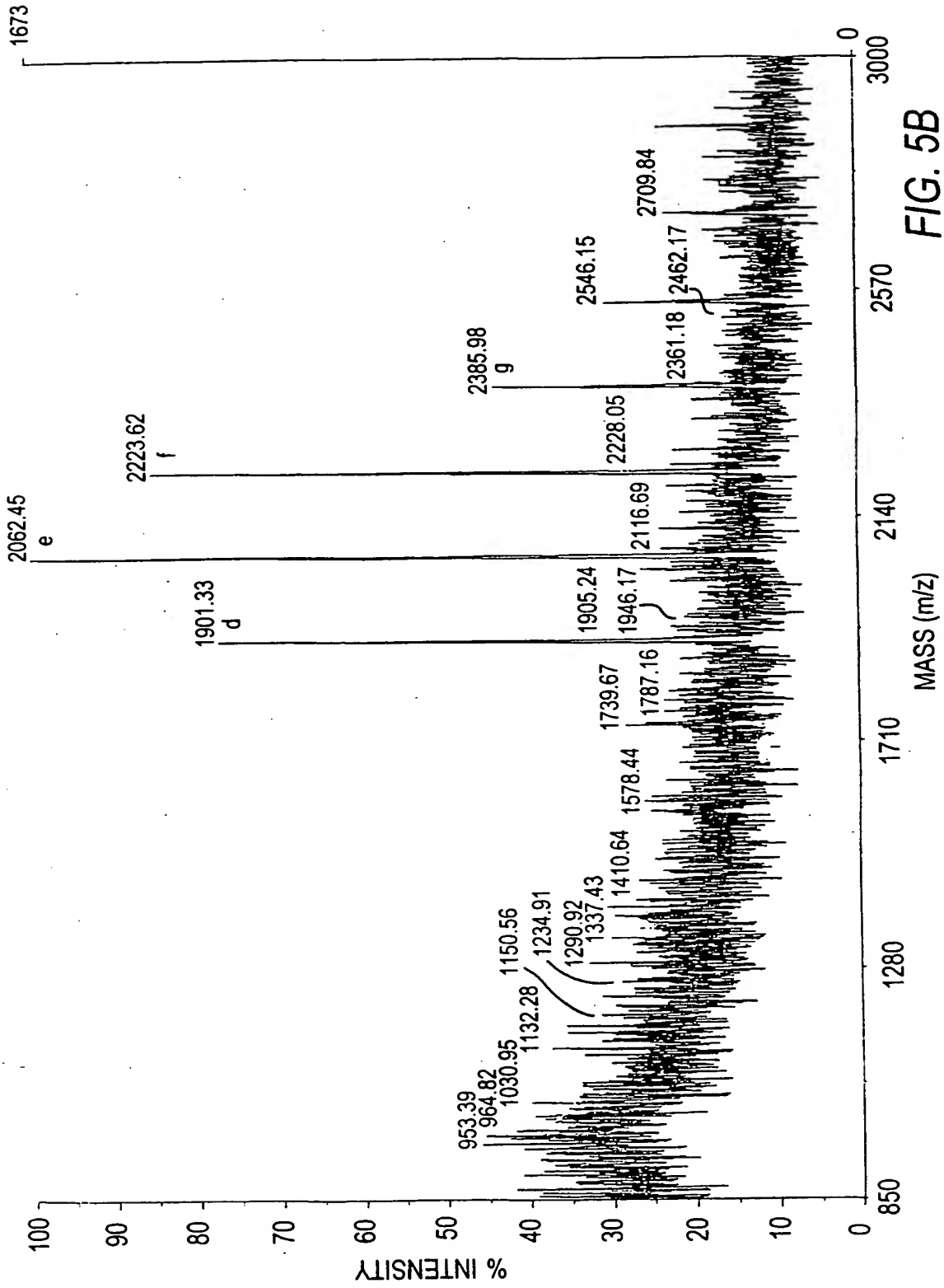

% INTENSITY
MASS (m/z)
100
90
80
70
60
50
40
30
20
10
0
850
1280
1710
2140
2570
3000
1673
2062.45
e
2223.62
f
2385.98
g
1901.33
d
2546.15
2709.84
2462.17
2361.18
2228.05
2116.69
1905.24
1946.17
1739.67
1787.16
1578.44
1410.64
1337.43
1290.92
1234.91
1150.56
1132.28
1030.95
964.82
953.39

FIG. 5B

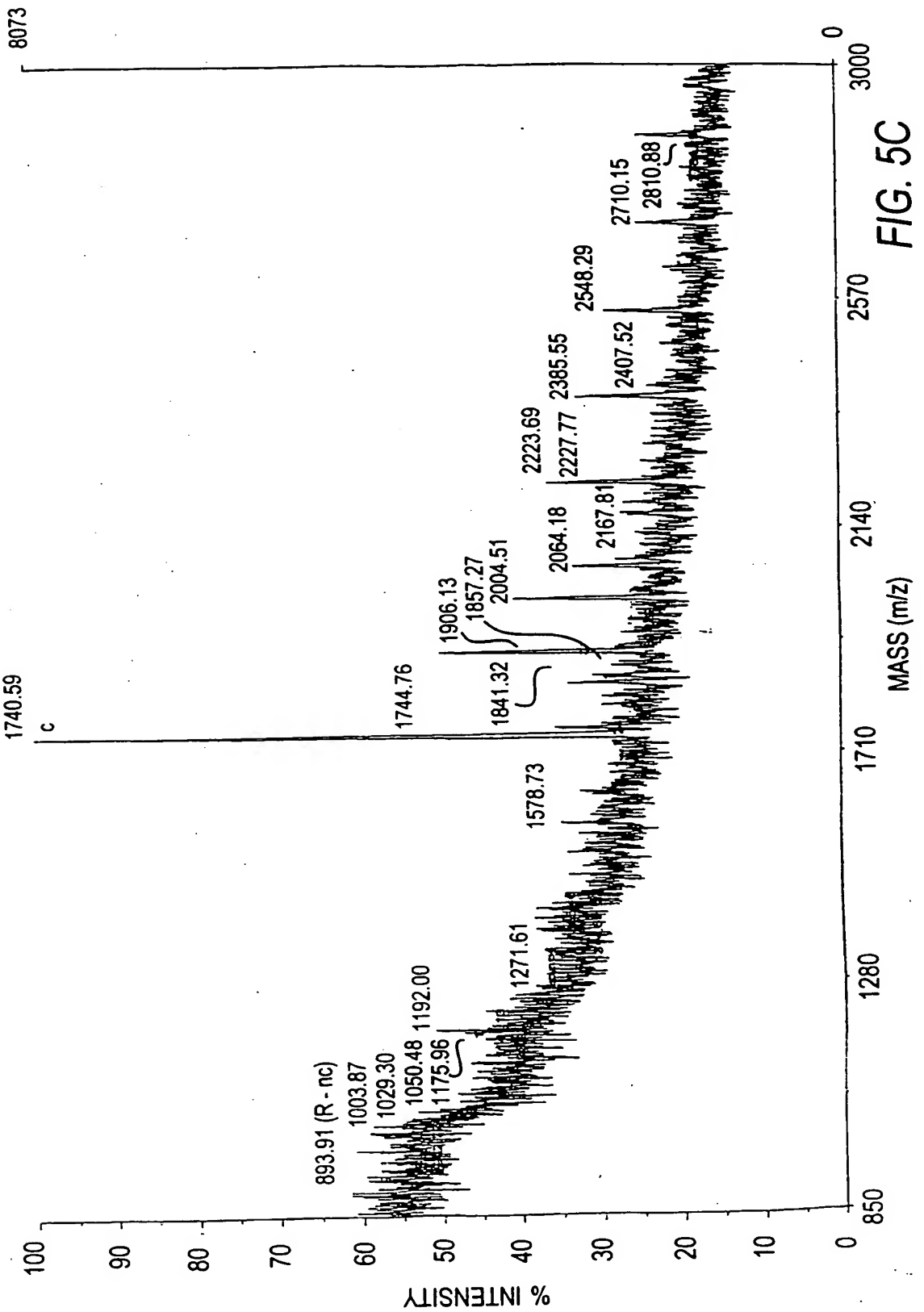

8073
0
3000
2570
2140
1710
1280
850
MASS (m/z)
% INTENSITY
100
90
80
70
60
50
40
30
20
10
0
1740.59
c
1744.76
1841.32
1906.13
1857.27
2004.51
2064.18
2167.81
2223.69
2227.77
2385.55
2407.52
2548.29
2710.15
2810.88
1578.73
1271.61
1192.00
1175.96
1050.48
1029.30
1003.87
893.91 (R - nc)

FIG. 5C

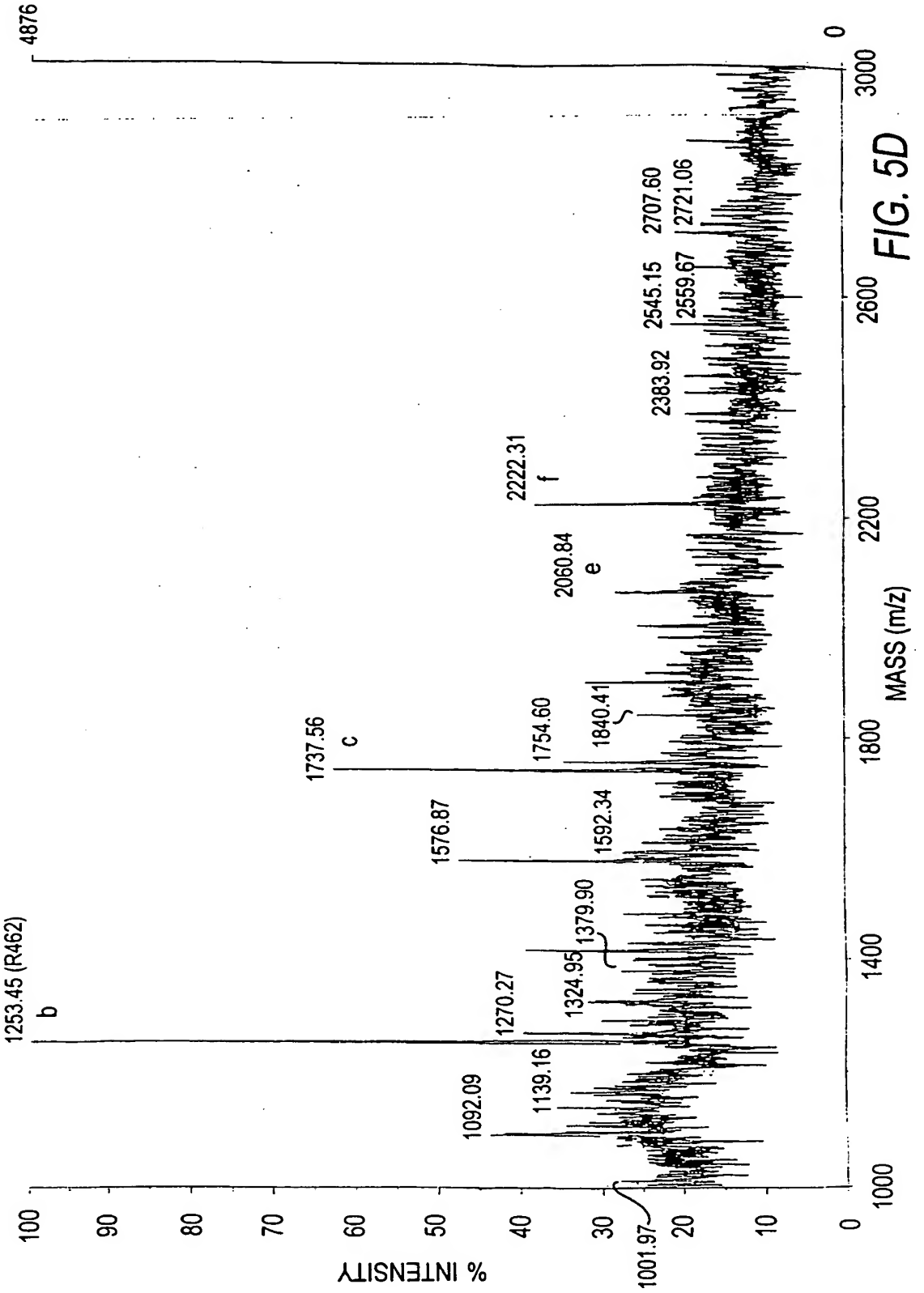

4876
0
3000
2600
2200
1800
1400
1000
MASS (m/z)
% INTENSITY
100
90
80
70
60
50
40
30
20
10
0
1001.97
1253.45 (R462)
b
1092.09
1139.16
1270.27
1324.95
1379.90
1576.87
1592.34
1737.56
c
1754.60
1840.41
2060.84
e
2222.31
f
2383.92
2545.15
2559.67
2707.60
2721.06

FIG. 5D

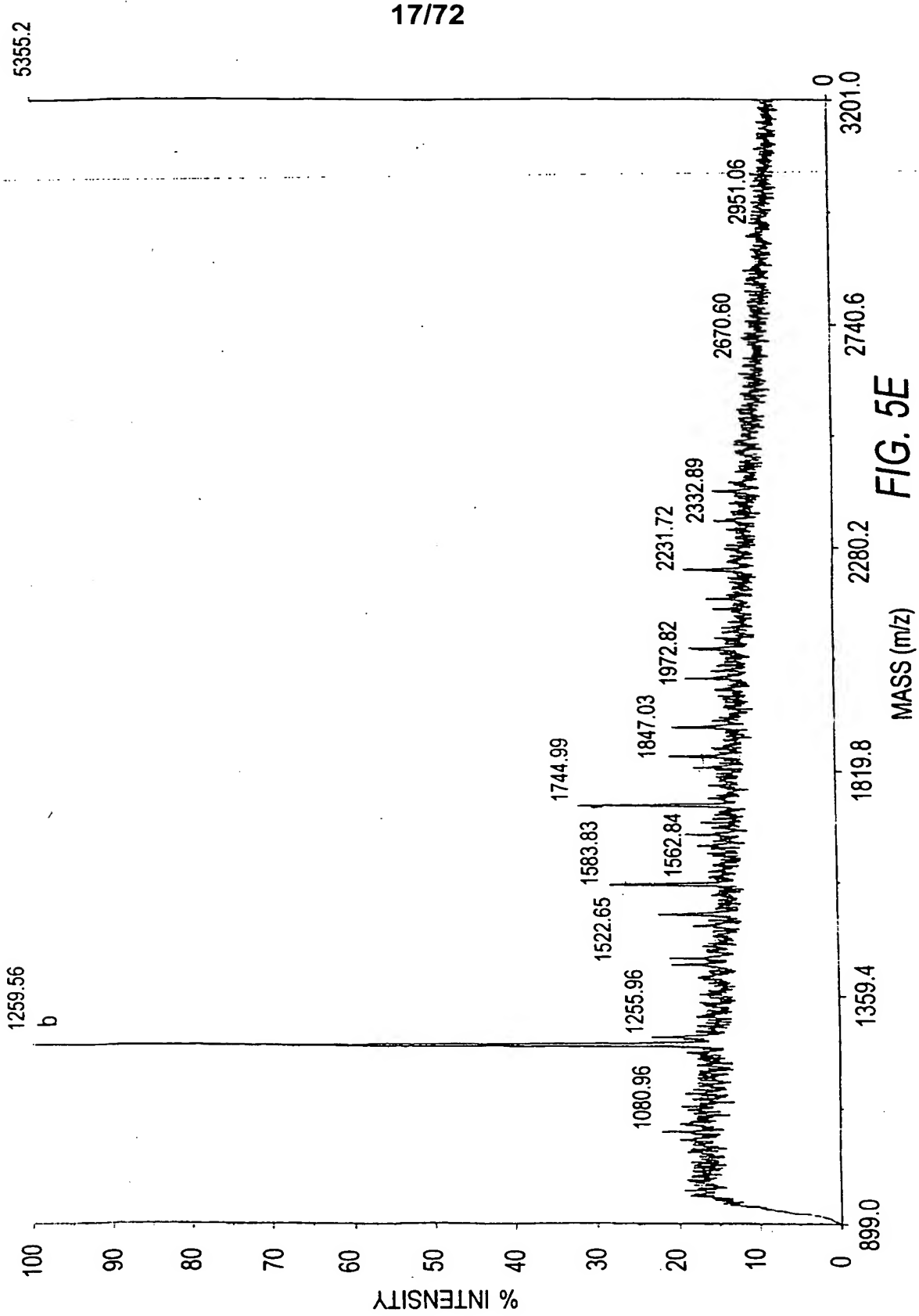

5355.2
0
3201.0
2951.06
2670.60
2740.6
2332.89
2231.72
2280.2
1972.82
1847.03
1744.99
1819.8
1583.83
1562.84
1522.65
1259.56
b
1255.96
1359.4
1080.96
899.0
0
10
20
30
40
50
60
70
80
90
100
% INTENSITY
MASS (m/z)

FIG. 5E

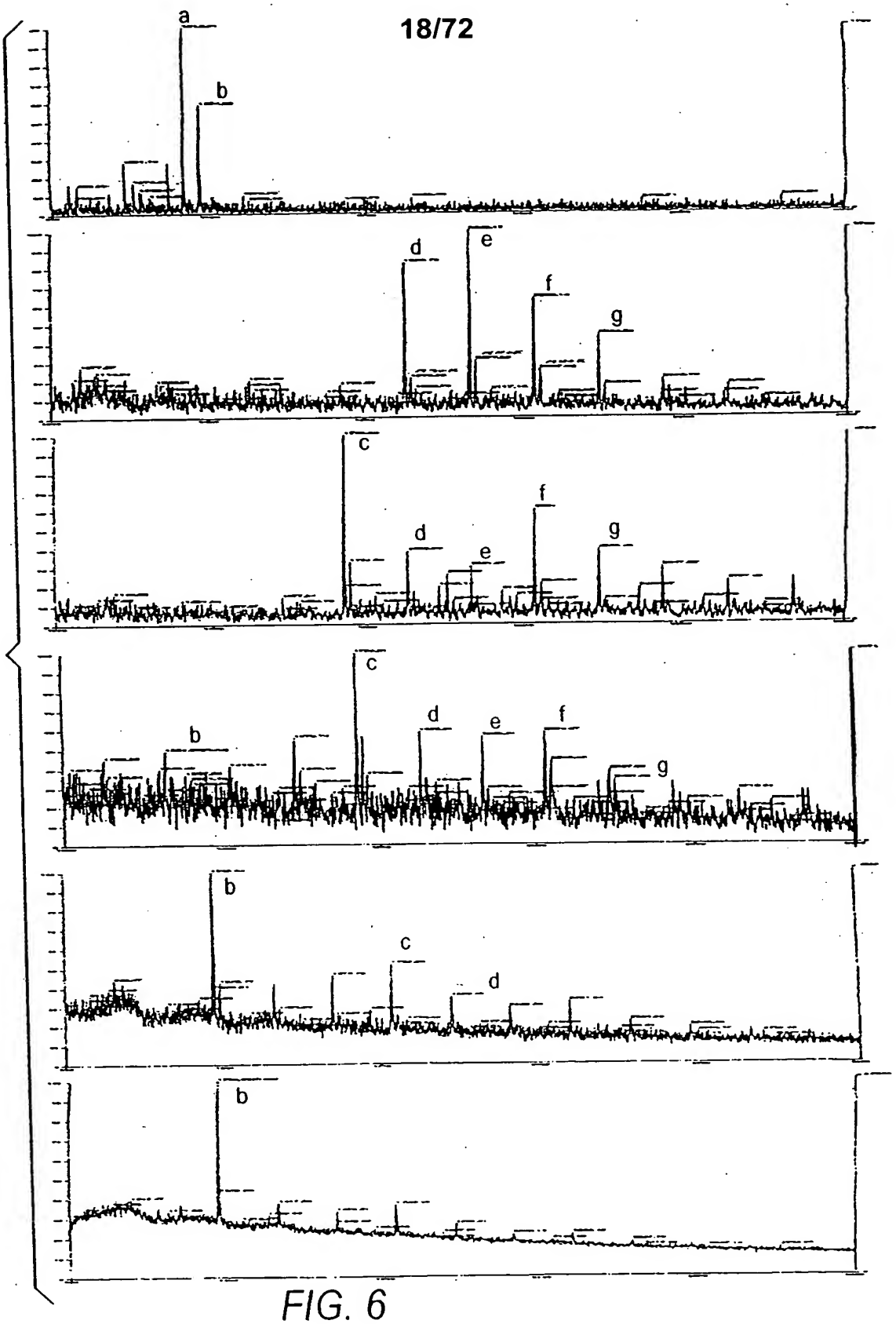


FIG. 6

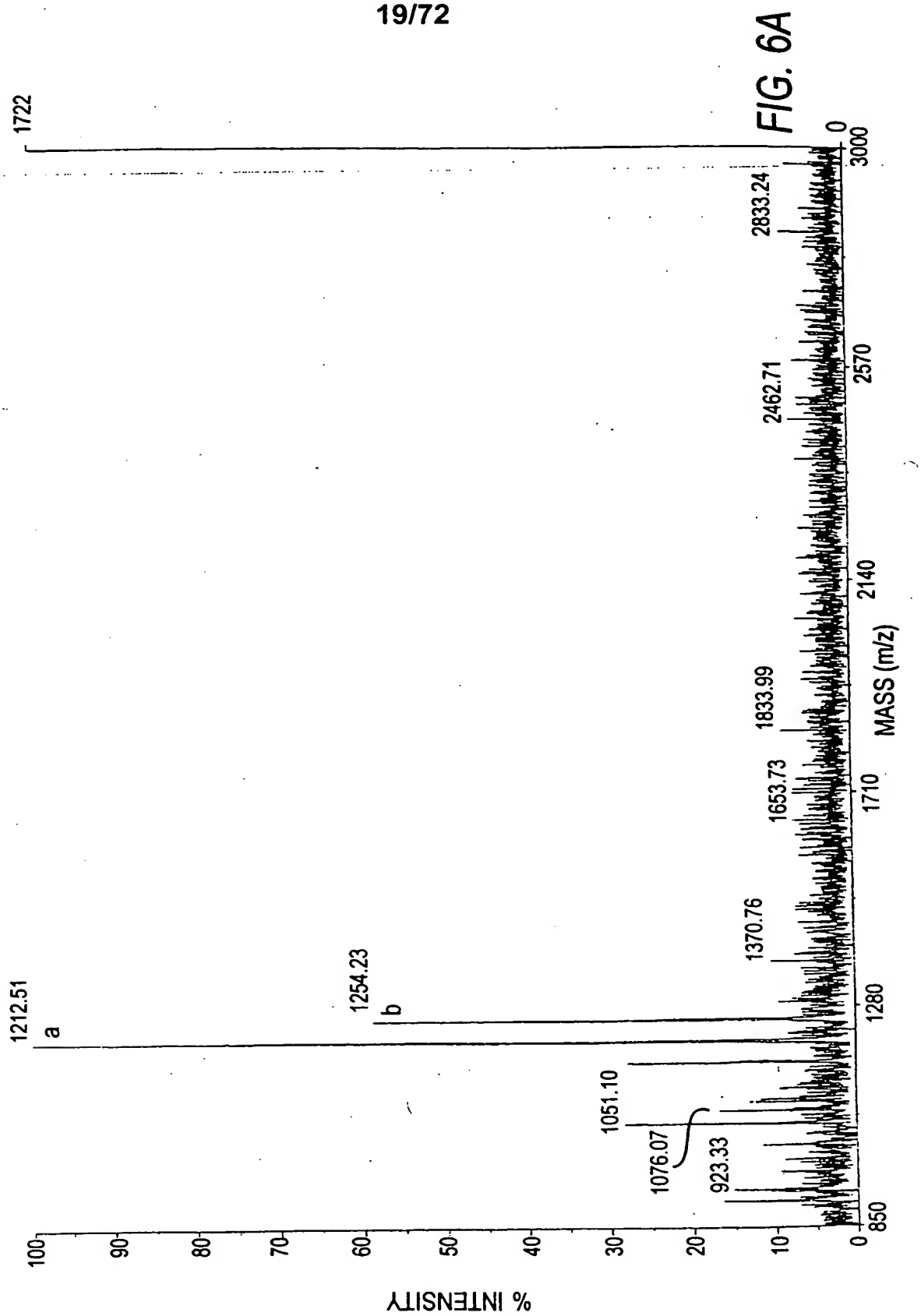

% INTENSITY
100
90
80
70
60
50
40
30
20
10
0
850
1280
1710
2140
2570
3000
MASS (m/z)
1212.51
a
1254.23
b
1722
1370.76
1653.73
1833.99
2462.71
2833.24
1051.10
1076.07
923.33

FIG. 6A

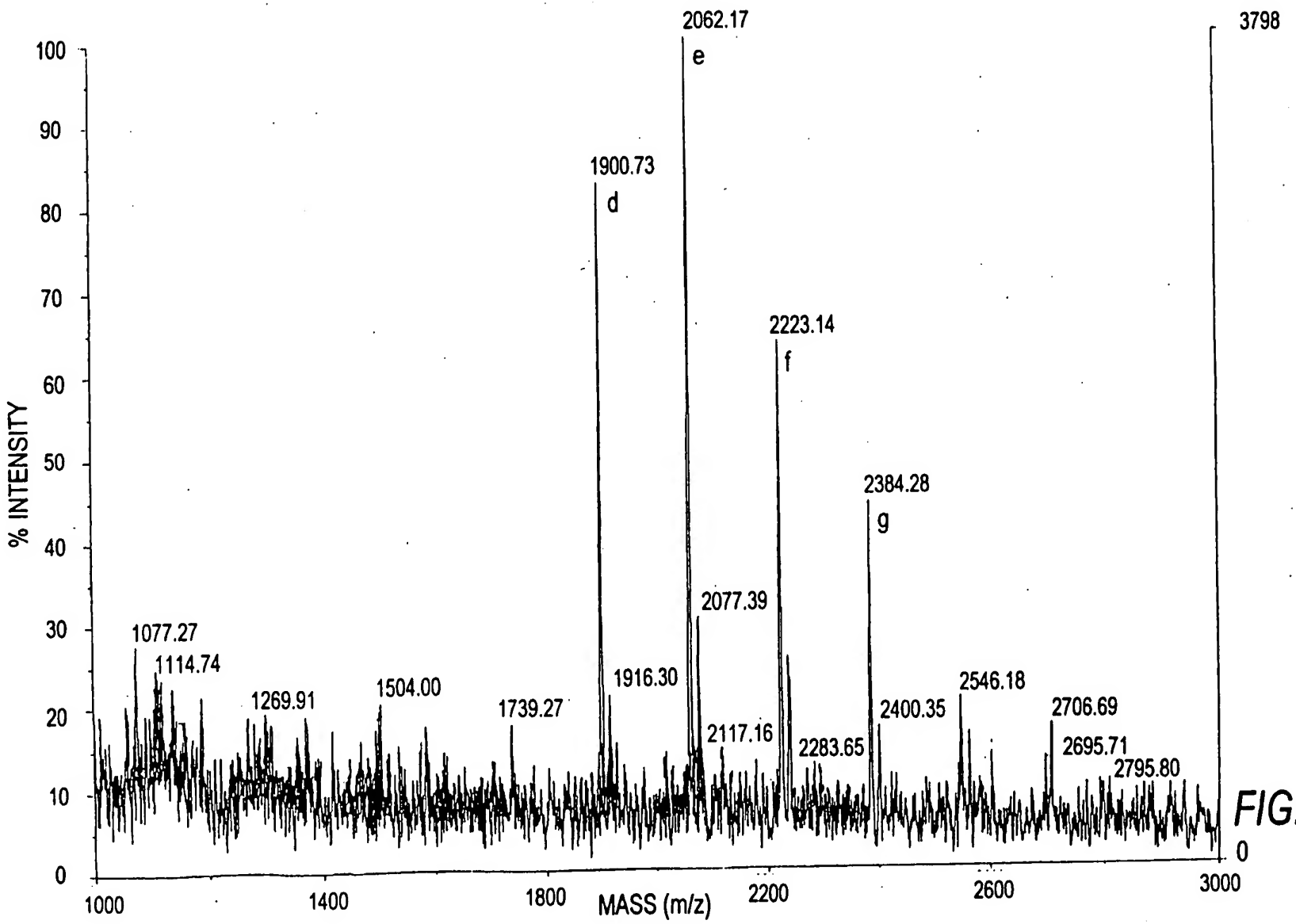

% INTENSITY
MASS (m/z)
100
90
80
70
60
50
40
30
20
10
0
1000
1400
1800
2200
2600
3000
2062.17
e
3798
1900.73
d
2223.14
f
2384.28
g
2077.39
1077.27
1114.74
1269.91
1504.00
1739.27
1916.30
2117.16
2283.65
2400.35
2546.18
2706.69
2695.71
2795.80

FIG. 6B

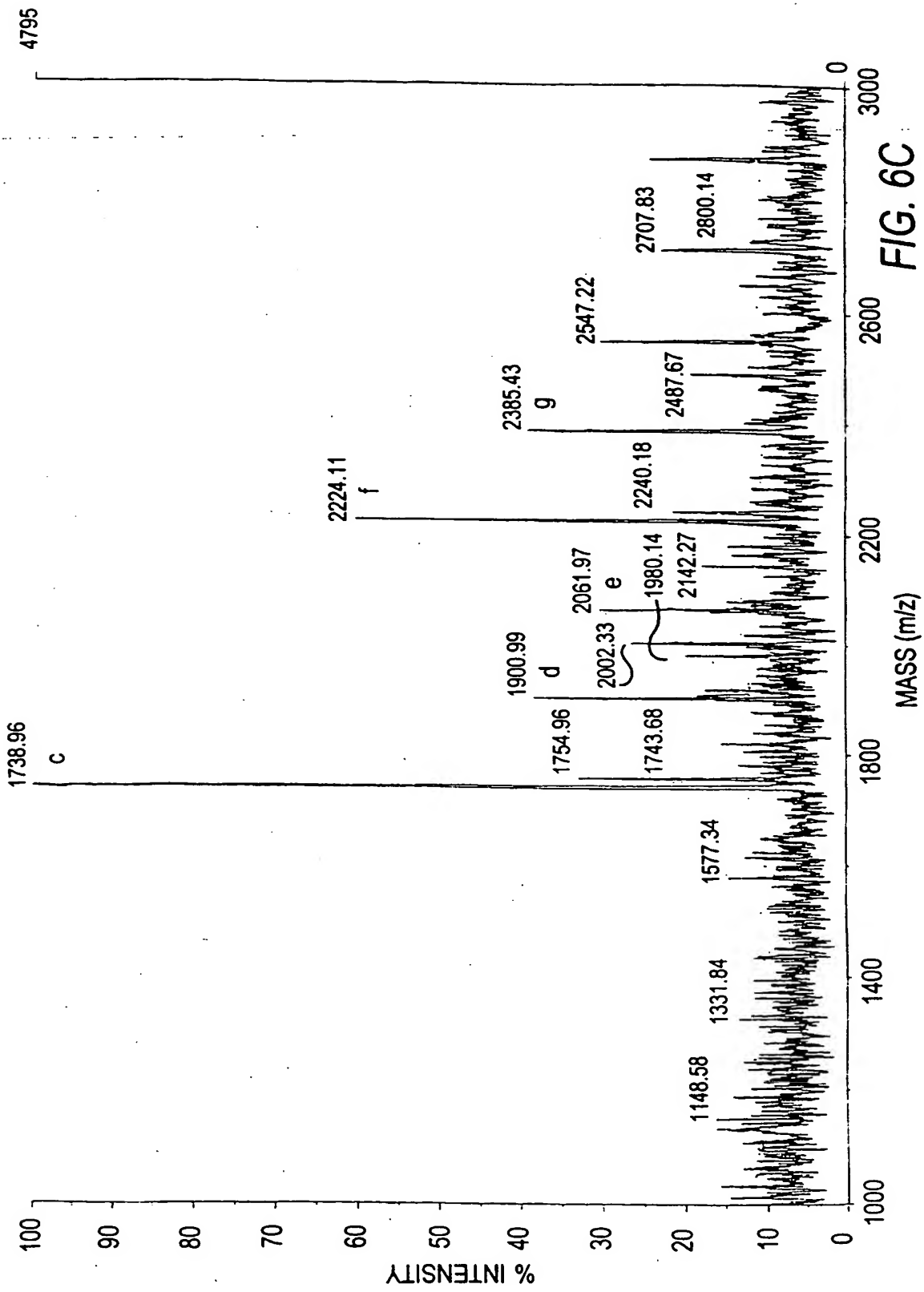

% INTENSITY
MASS (m/z)
1738.96
c
1754.96
1743.68
1900.99
d
2002.33
2061.97
e
1980.14
2142.27
2224.11
f
2240.18
2385.43
g
2487.67
2547.22
2707.83
2800.14
4795
1148.58
1331.84
1577.34

FIG. 6C

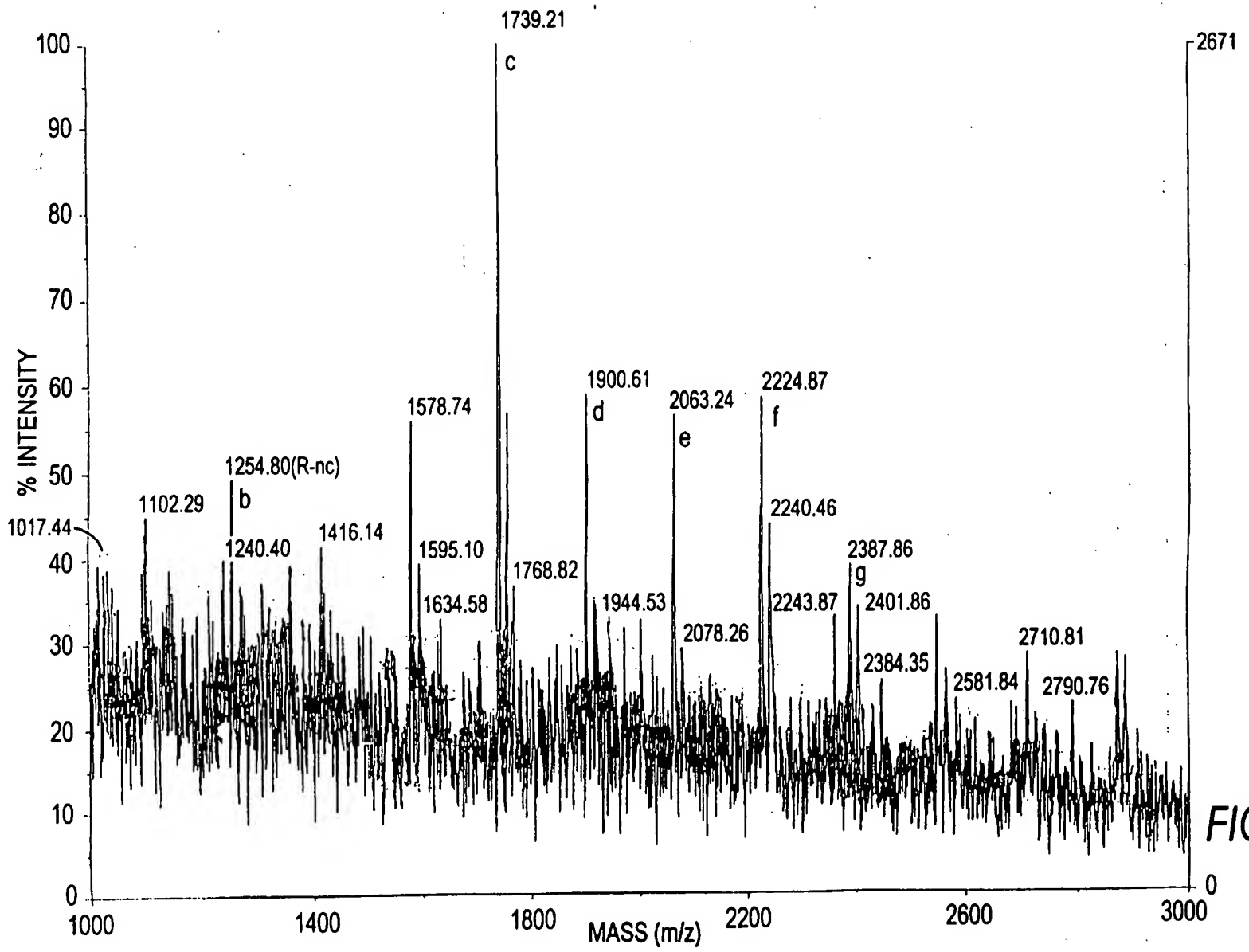

% INTENSITY
MASS (m/z)
100
90
80
70
60
50
40
30
20
10
0
1000
1400
1800
2200
2600
3000
1739.21
c
2671
1900.61
d
2063.24
e
2224.87
f
1578.74
1254.80(R-nc)
b
1102.29
1017.44
1240.40
1416.14
1595.10
1634.58
1768.82
1944.53
2078.26
2240.46
2243.87
2387.86
g
2401.86
2384.35
2710.81
2581.84
2790.76

FIG. 6D

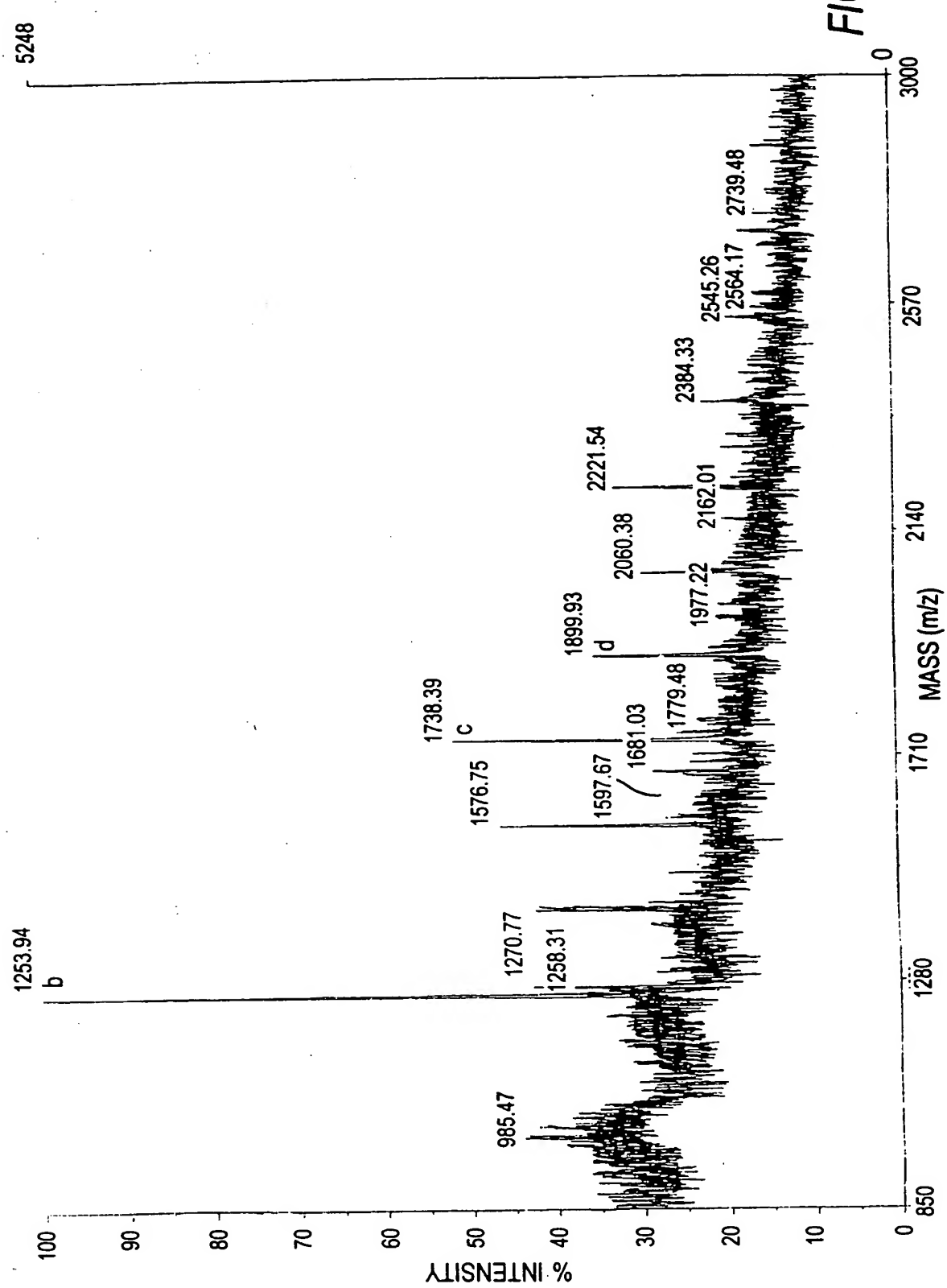

5248
1253.94
b
1270.77
1258.31
985.47
1738.39
c
1576.75
1597.67
1681.03
1899.93
d
1779.48
1977.22
2060.38
2221.54
2162.01
2384.33
2545.26
2564.17
2739.48
% INTENSITY
MASS (m/z)
100
90
80
70
60
50
40
30
20
10
0
850
1280
1710
2140
2570
3000
0

FIG. 6E

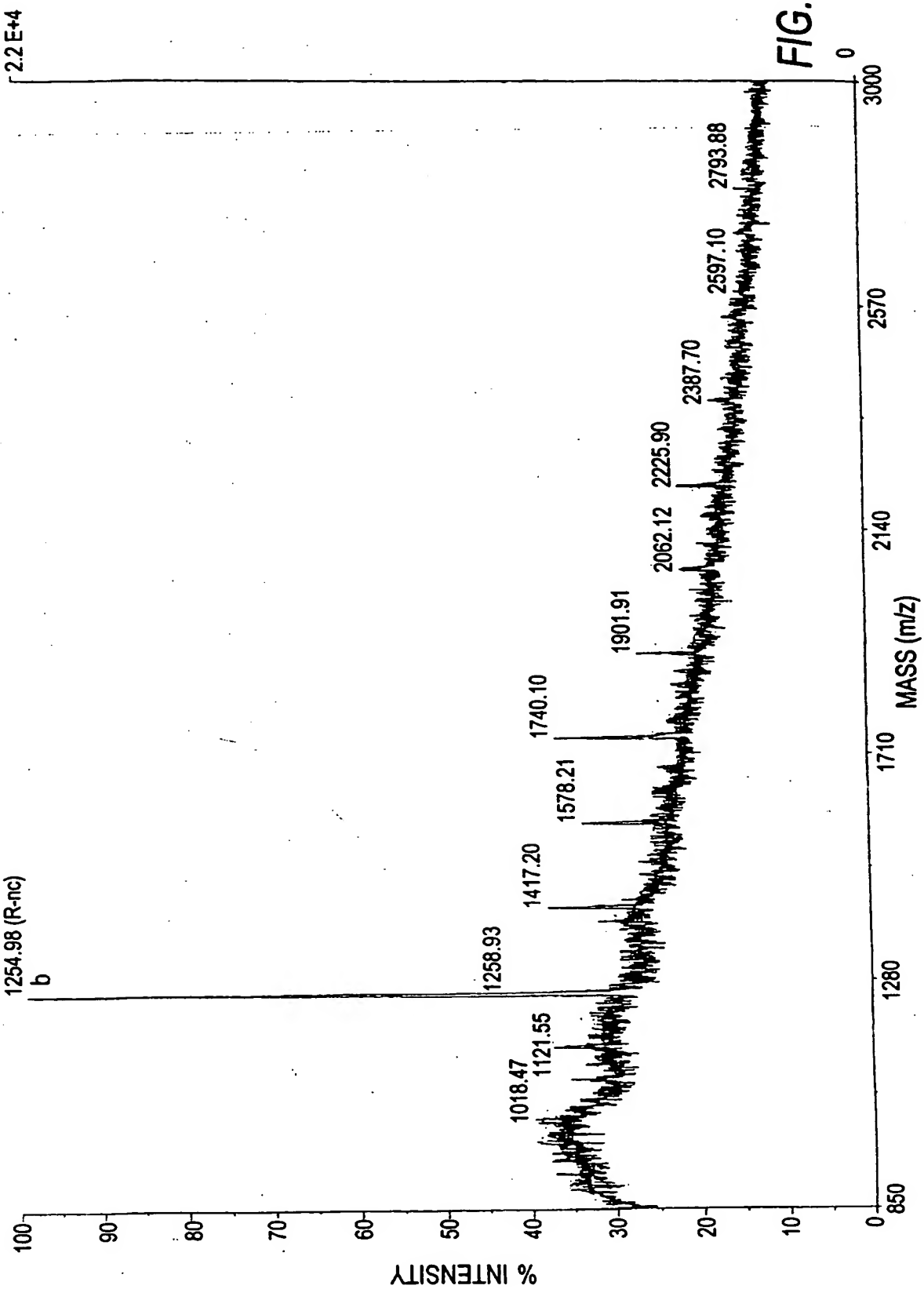

2.2 E+4
0
% INTENSITY
100
90
80
70
60
50
40
30
20
10
0
850
1280
1710
2140
2570
3000
MASS (m/z)
1254.98 (R-nc)
b
1258.93
1417.20
1578.21
1740.10
1901.91
2062.12
2225.90
2387.70
2597.10
2793.88
1018.47
1121.55

FIG. 6F

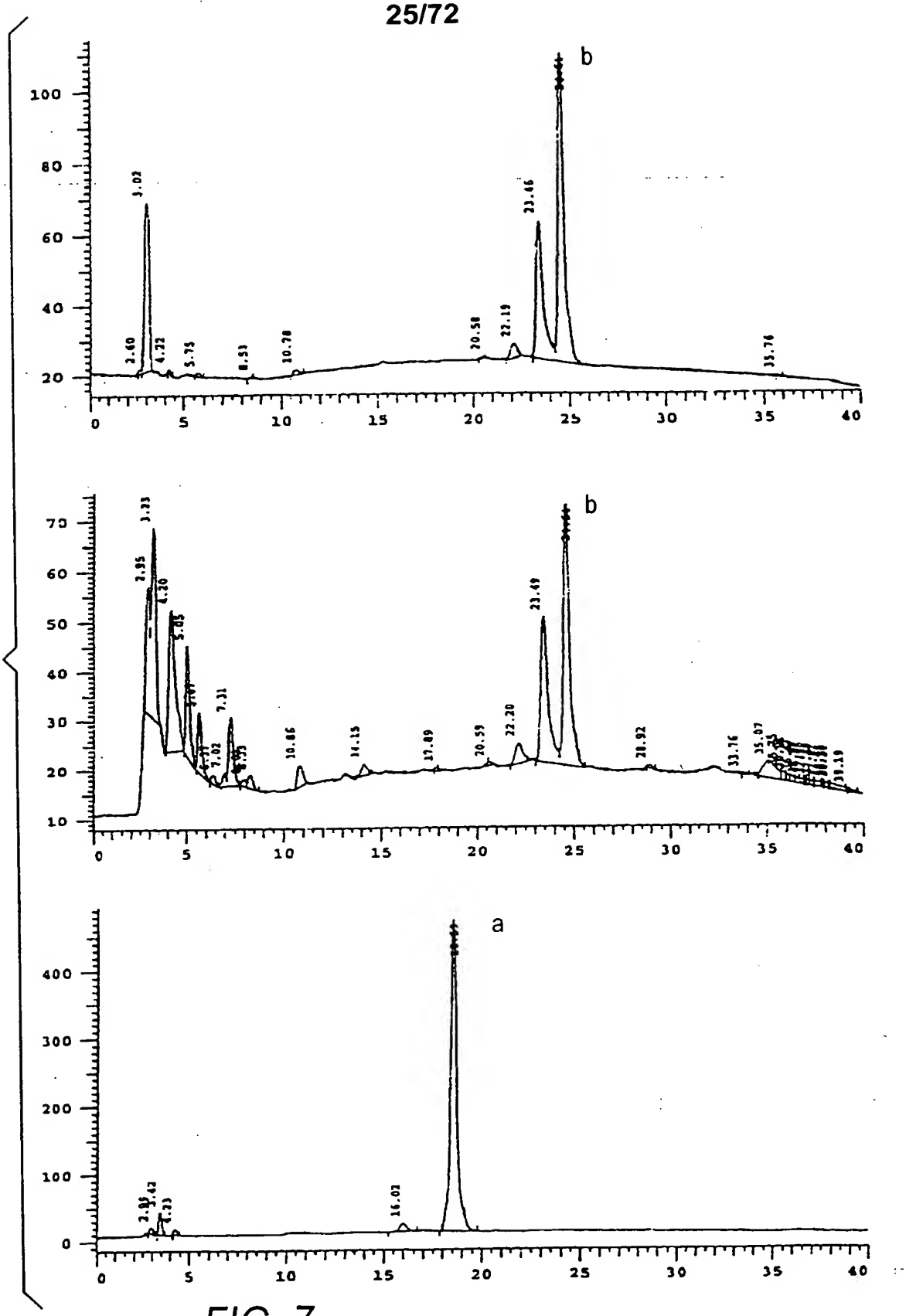


FIG. 7

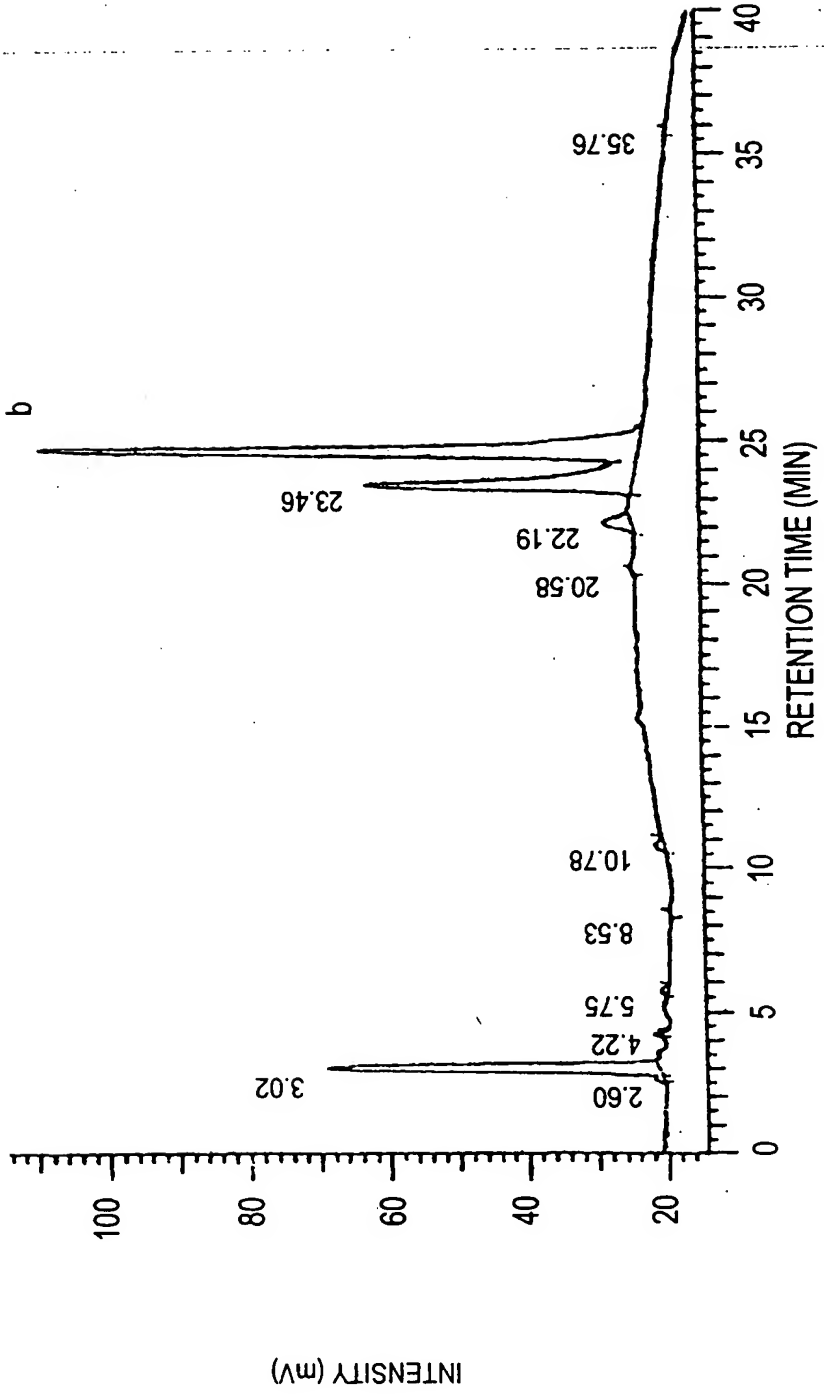

INTENSITY (mV)
100
80
60
40
20
0
5
10
15
20
25
30
35
40
RETENTION TIME (MIN)
3.02
2.60
4.22
5.75
8.53
10.78
20.58
22.19
23.46
35.76
b

FIG. 7A

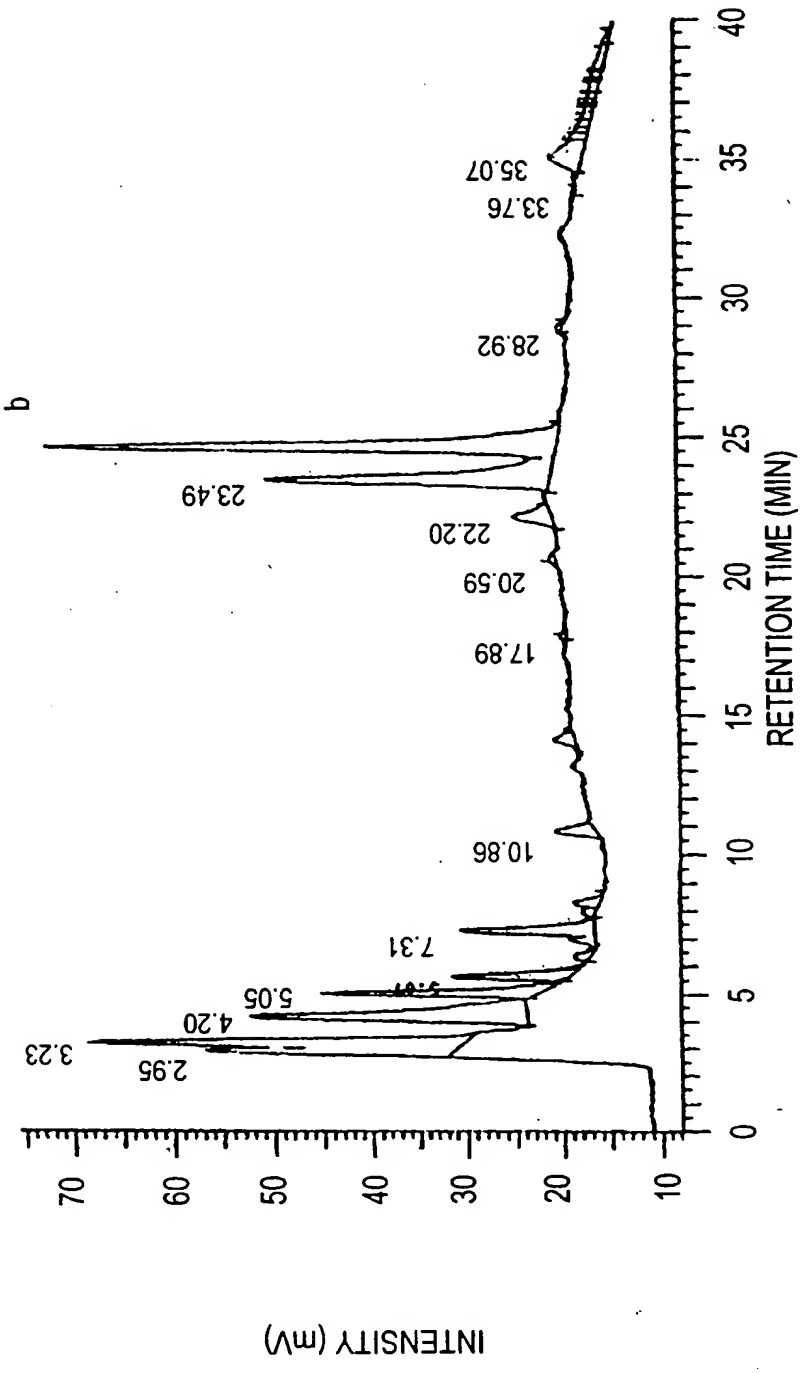

INTENSITY (mV)
70
60
50
40
30
20
10
0
5
10
15
20
25
30
35
40
RETENTION TIME (MIN)
b
2.95
3.23
4.20
5.05
7.31
10.86
17.89
20.59
22.20
23.49
28.92
33.76
35.07

FIG. 7B

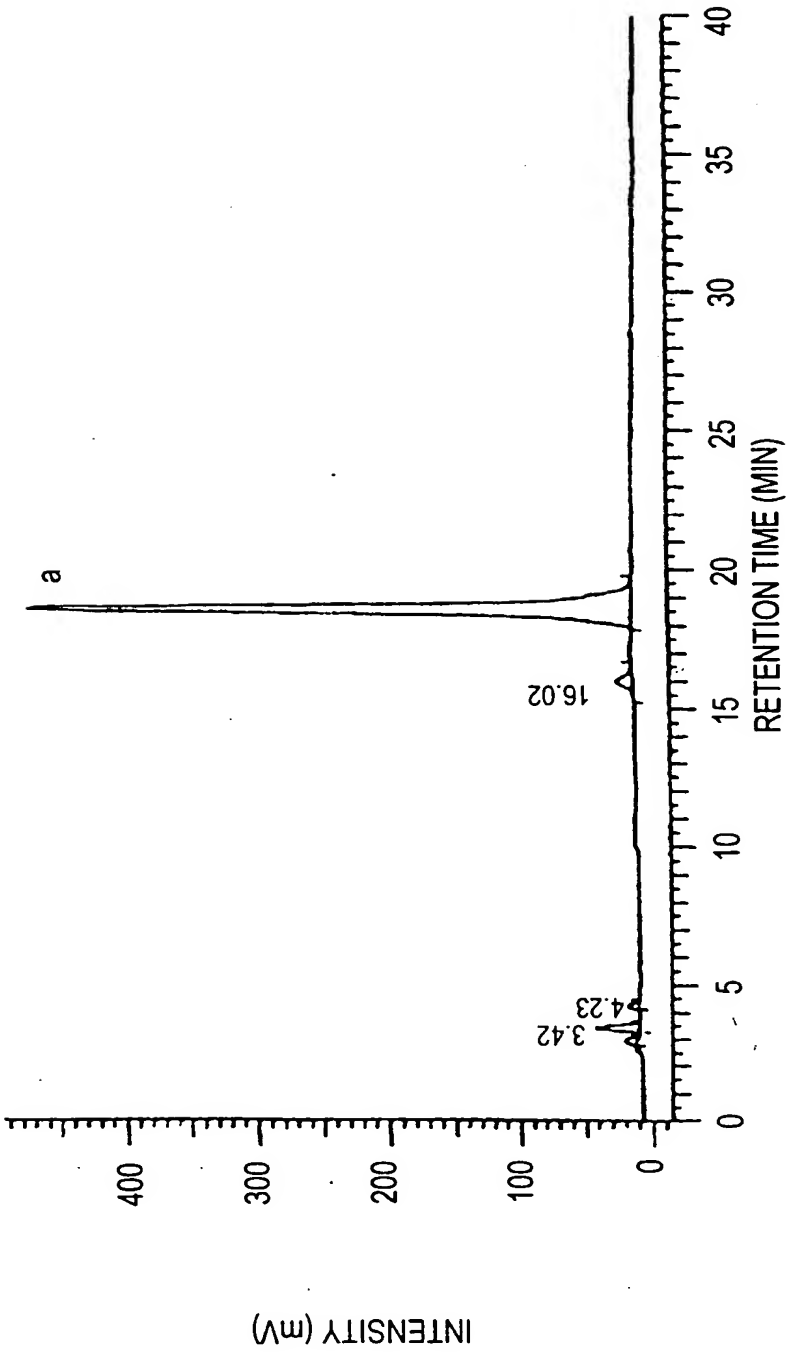

INTENSITY (mV)
400
300
200
100
0
0
5
10
15
20
25
30
35
40
RETENTION TIME (MIN)
3.42
4.23
16.02
a

FIG. 7C

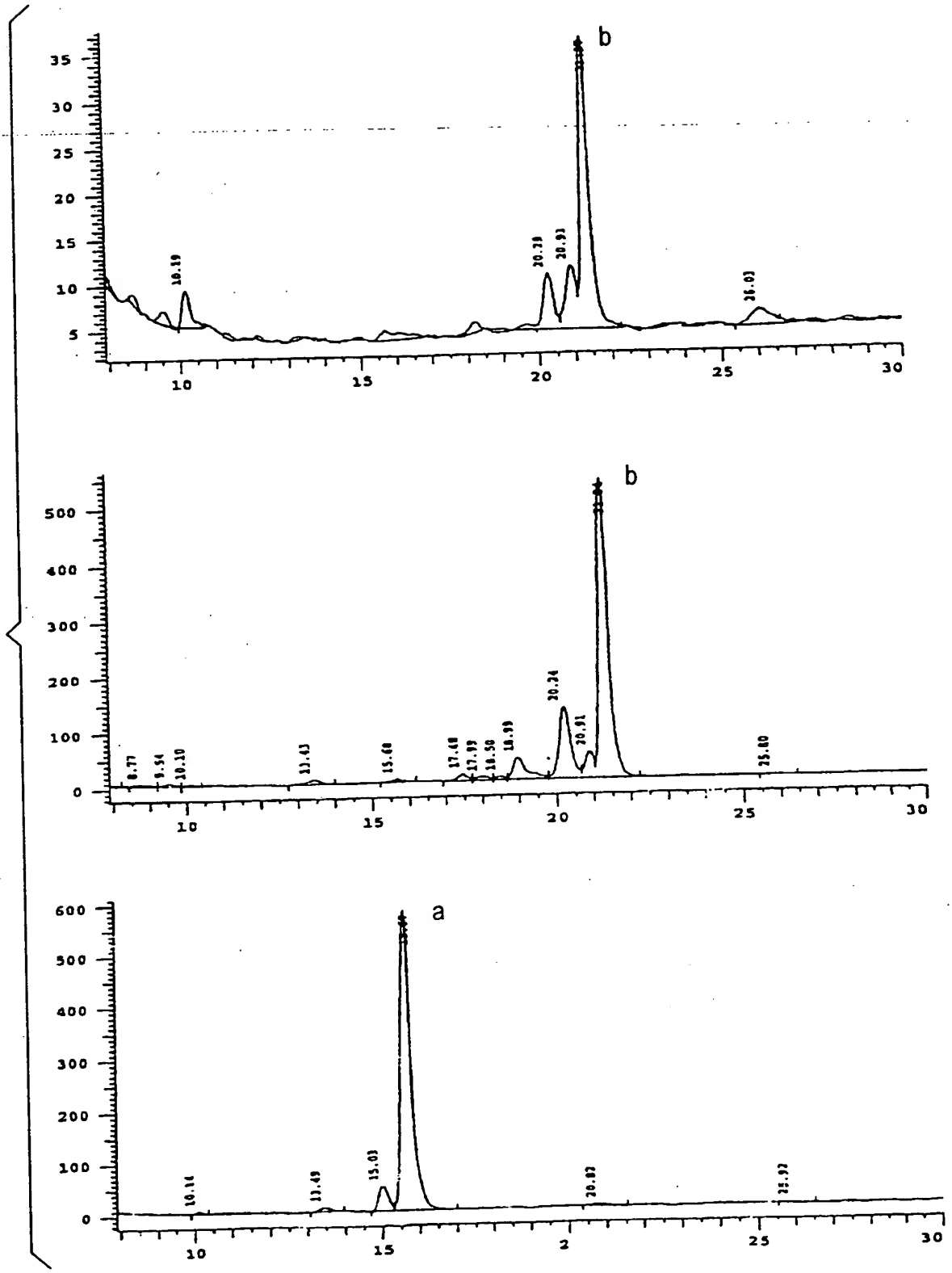


FIG. 8

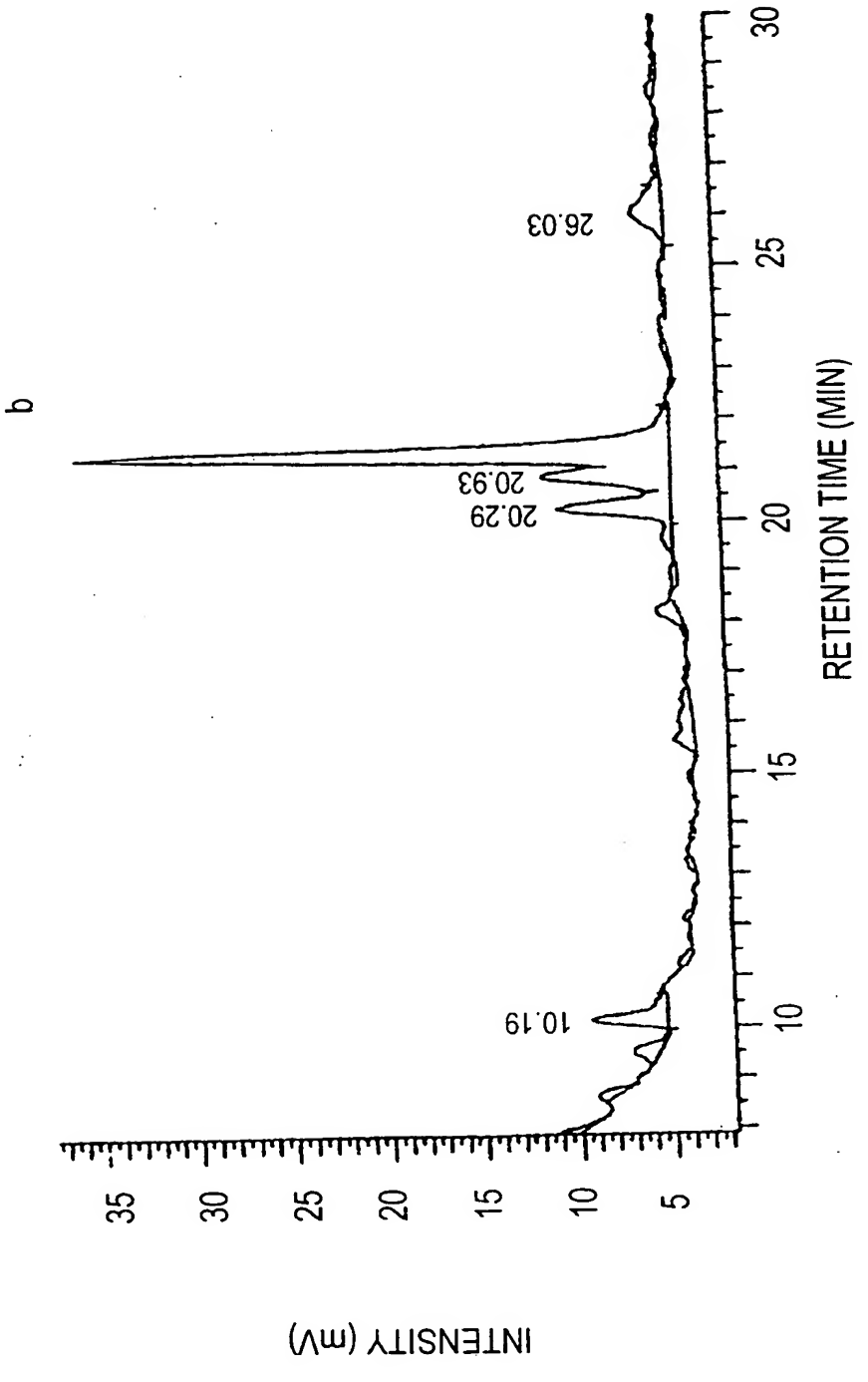


FIG. 8A

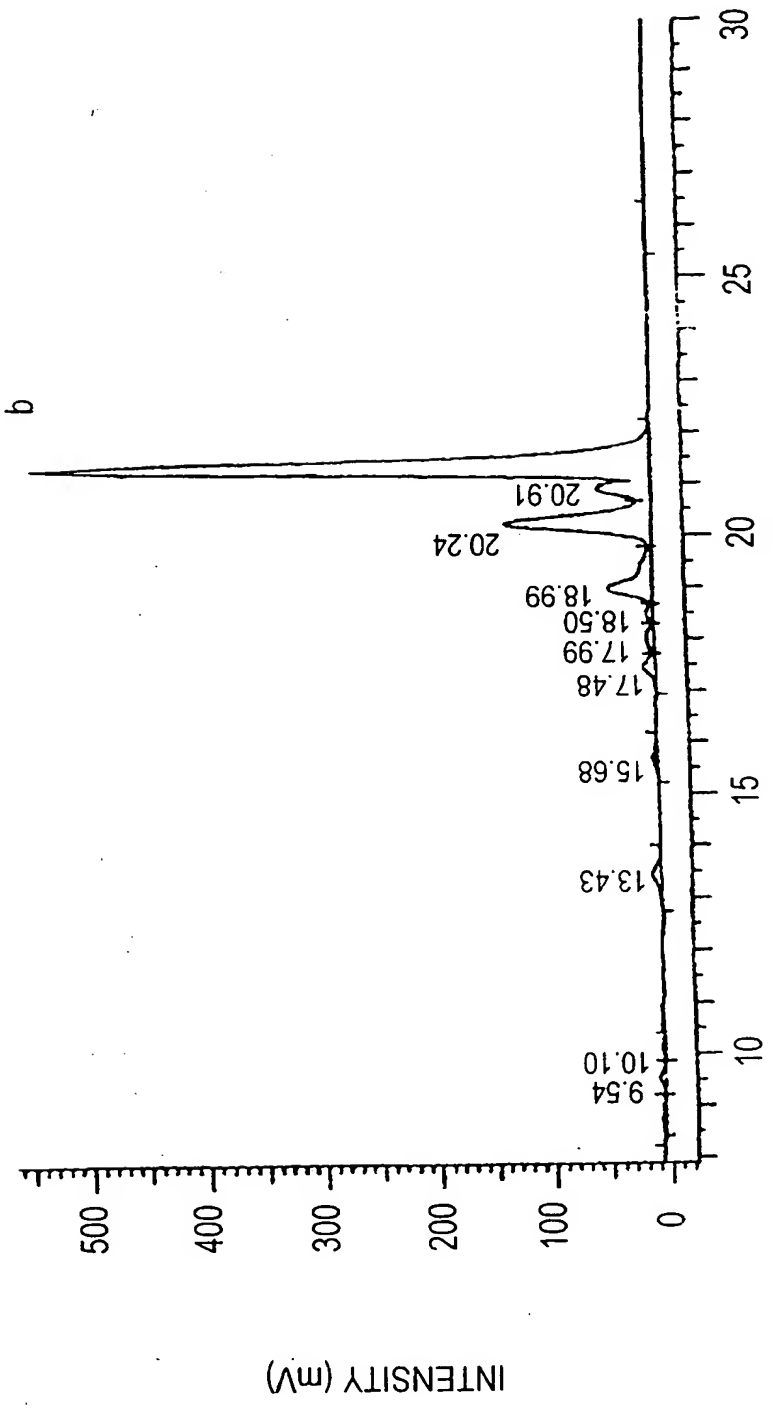

b
9.54
10.10
13.43
15.68
17.48
17.99
18.50
18.99
20.24
20.91
0
100
200
300
400
500
10
15
20
25
30
INTENSITY (mV)
RETENTION TIME (MIN)

FIG. 8B

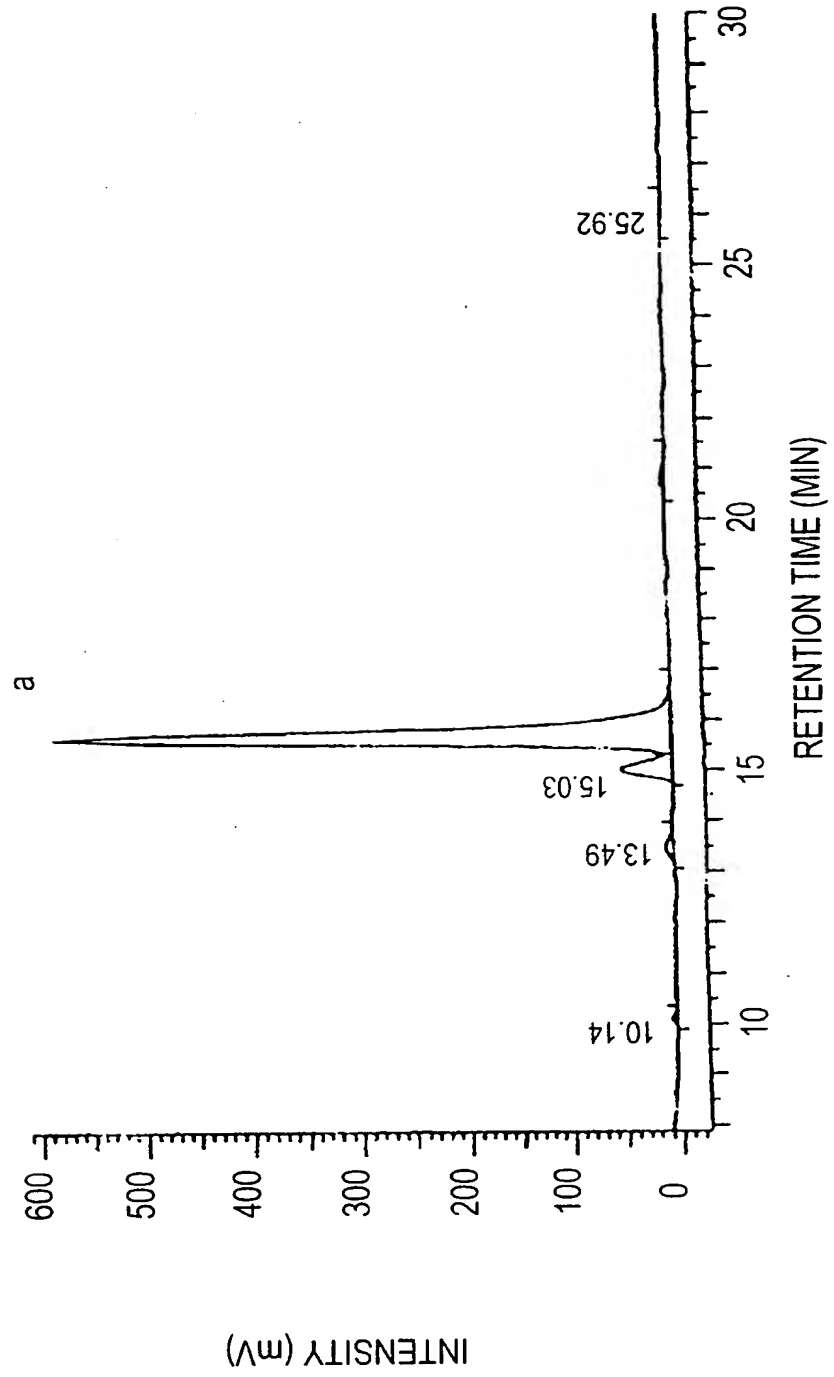

INTENSITY (mV)
600
500
400
300
200
100
0
10.14
13.49
15.03
25.92
a
10
15
20
25
30
RETENTION TIME (MIN)

FIG. 8C

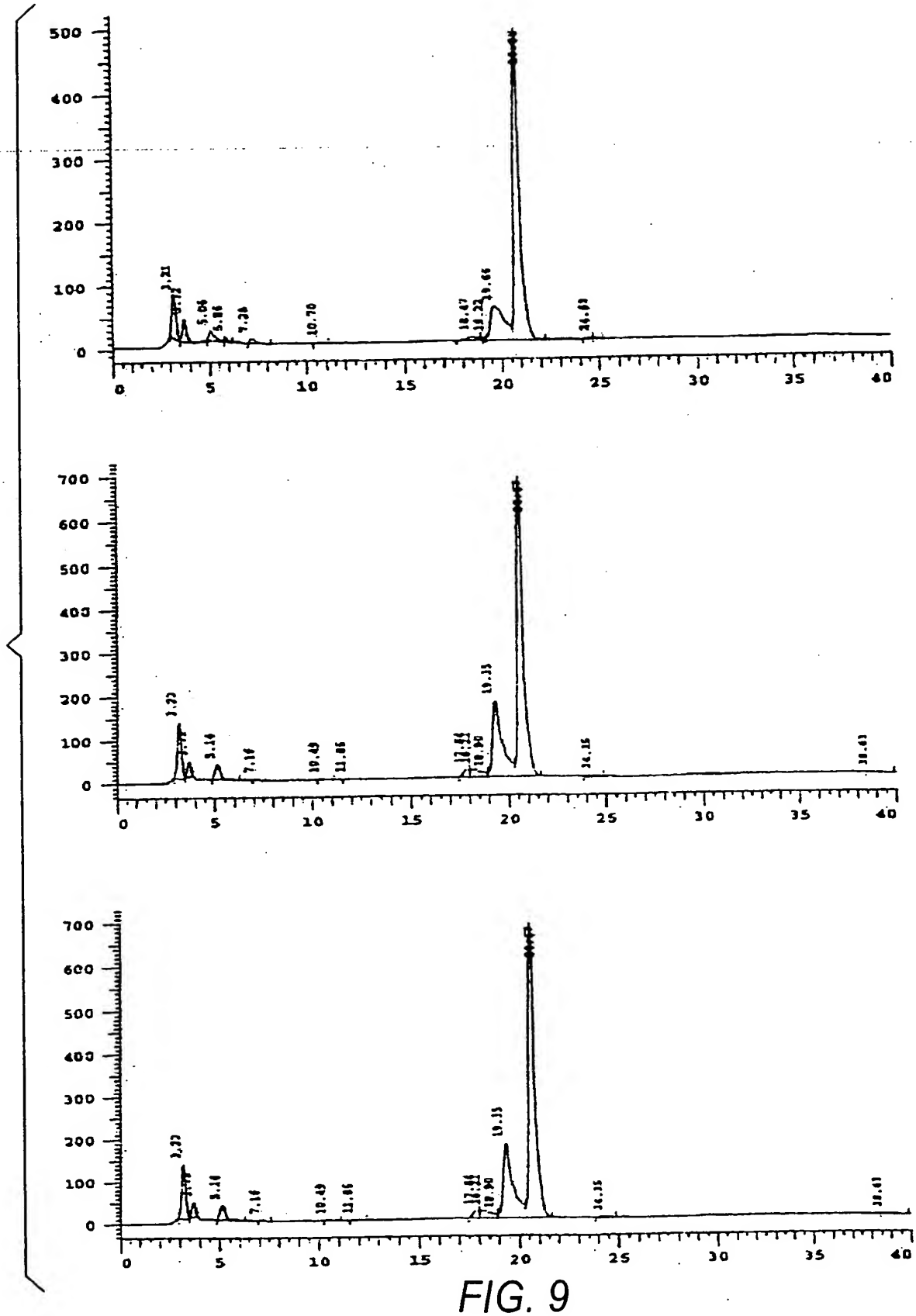

500
400
300
200
100
0
0
5
10
15
20
25
30
35
40
700
600
500
400
300
200
100
0
0
5
10
15
20
25
30
35
40
700
600
500
400
300
200
100
0
0
5
10
15
20
25
30
35
40

FIG. 9

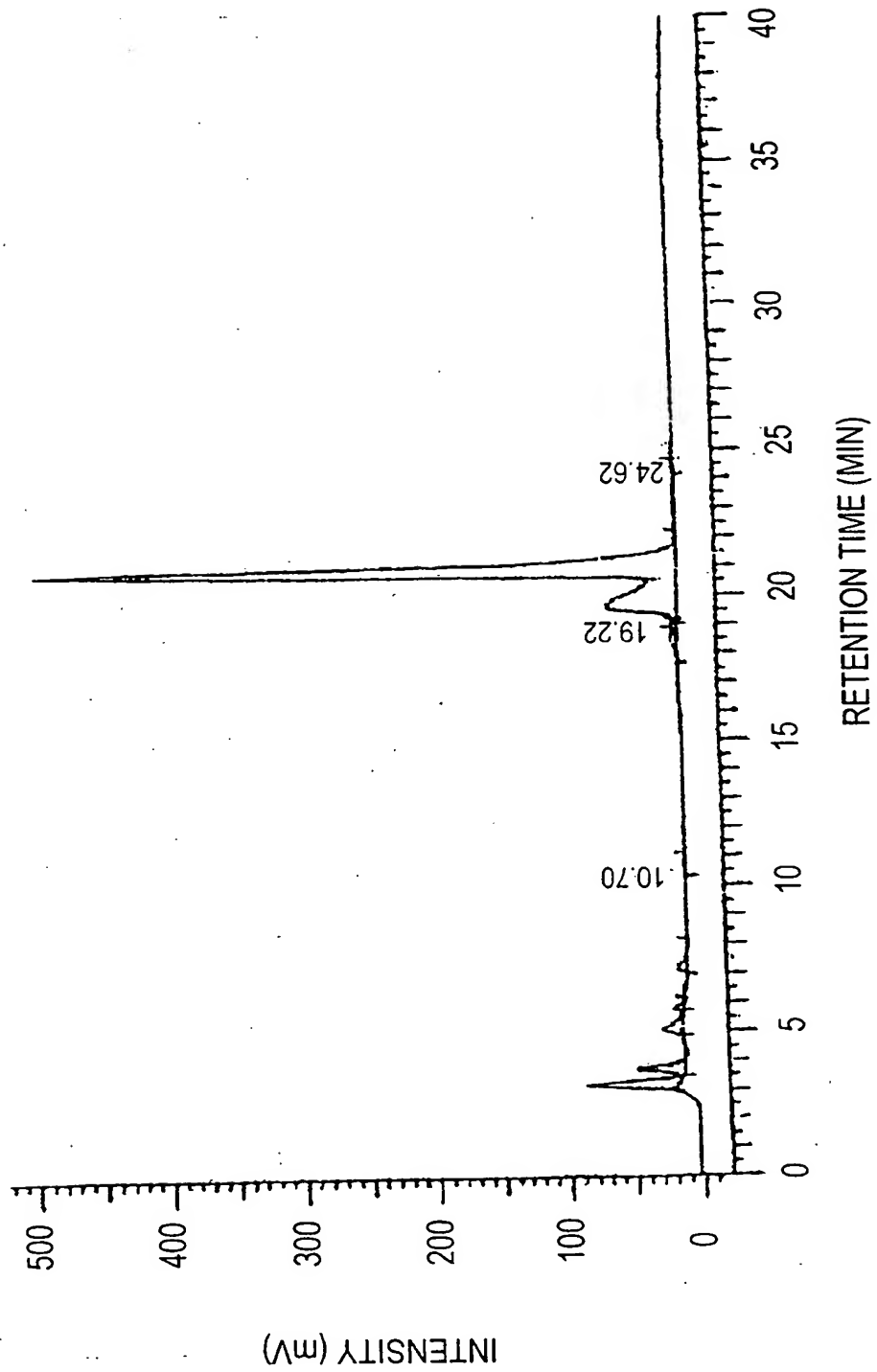

INTENSITY (mV)
500
400
300
200
100
0
0
5
10
15
20
25
30
35
40
RETENTION TIME (MIN)
10.70
19.22
24.62

FIG. 9A

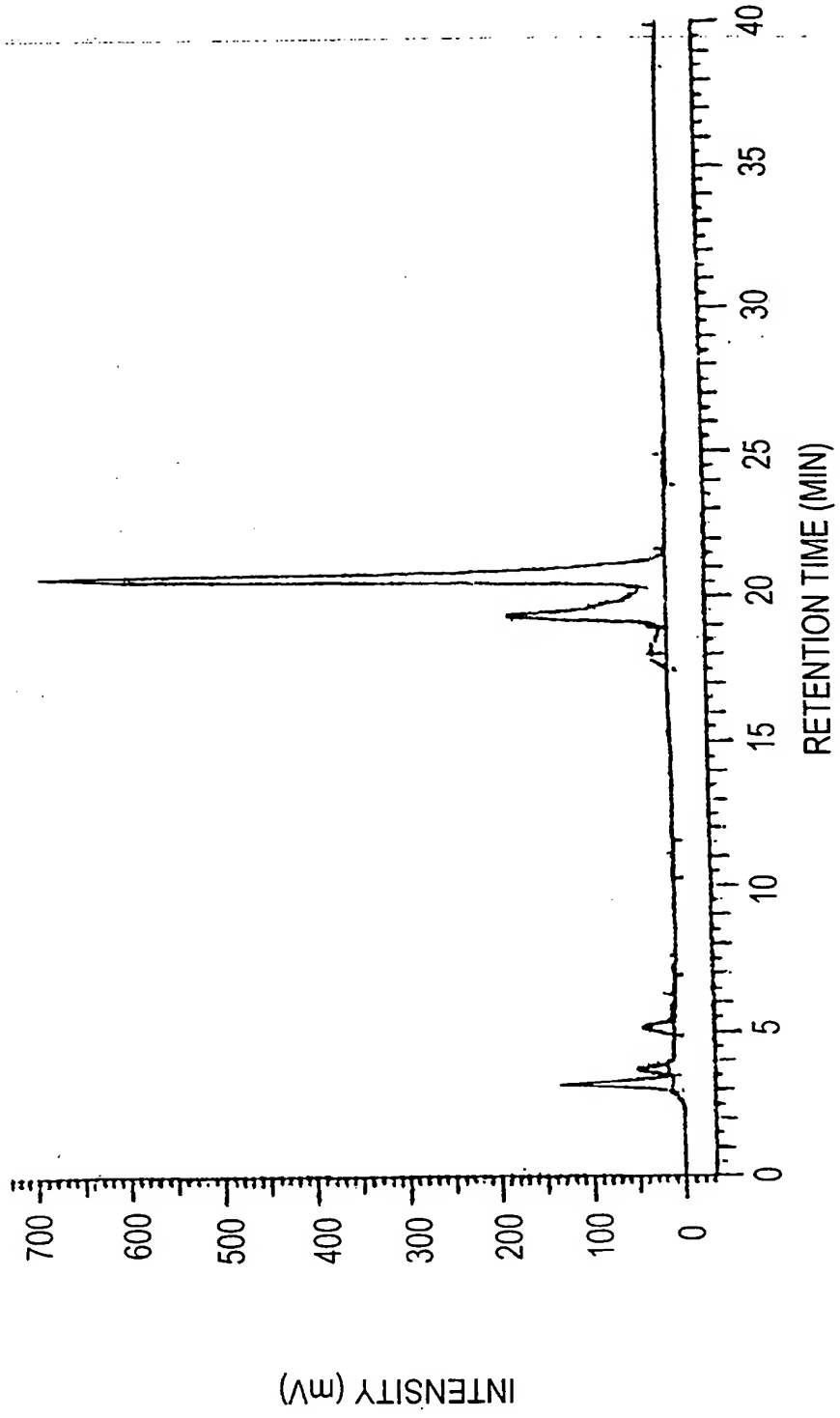

INTENSITY (mV)
700
600
500
400
300
200
100
0
0
5
10
15
20
25
30
35
40
RETENTION TIME (MIN)

FIG. 9B

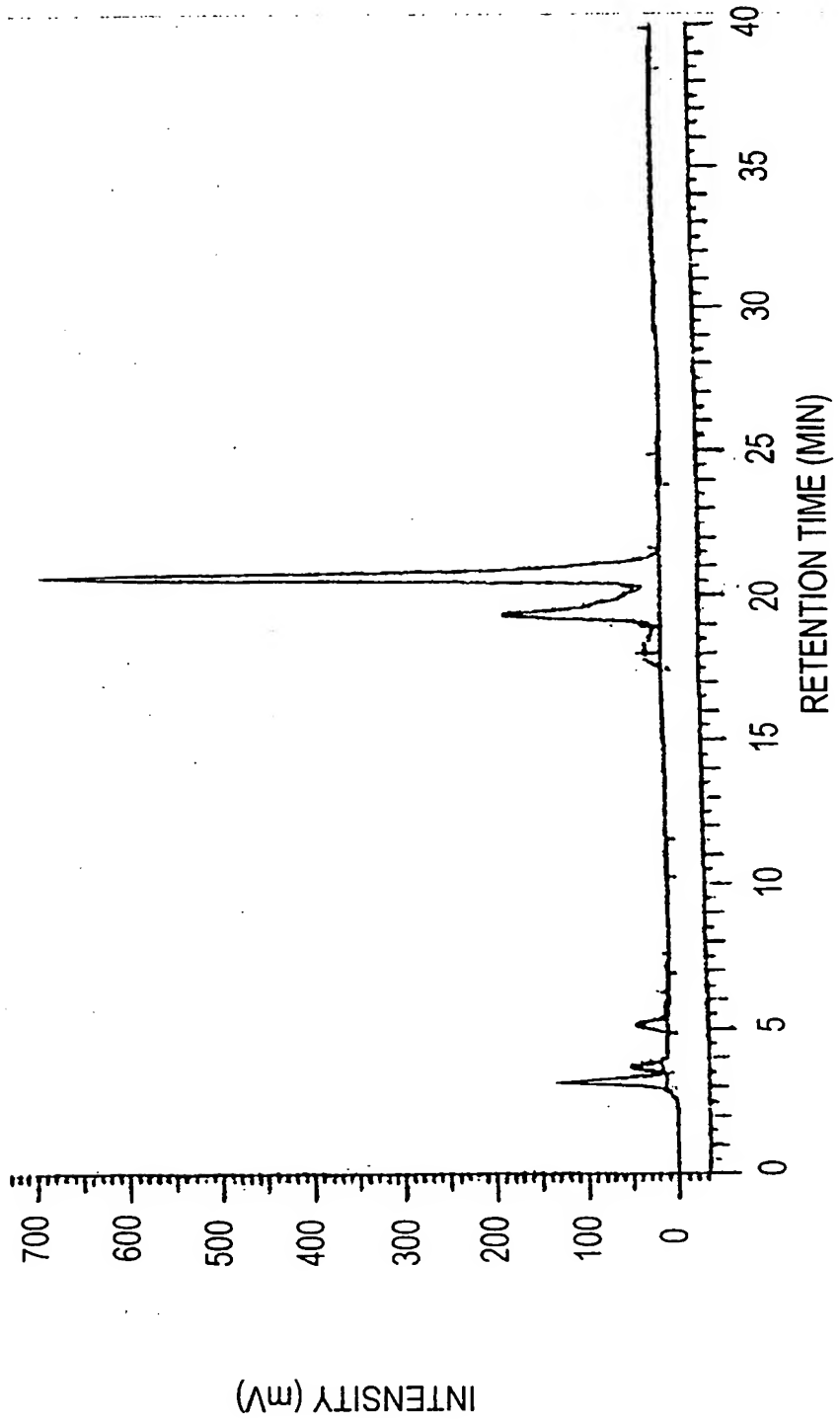

INTENSITY (mV)
700
600
500
400
300
200
100
0
0
5
10
15
20
25
30
35
40
RETENTION TIME (MIN)

FIG. 9C

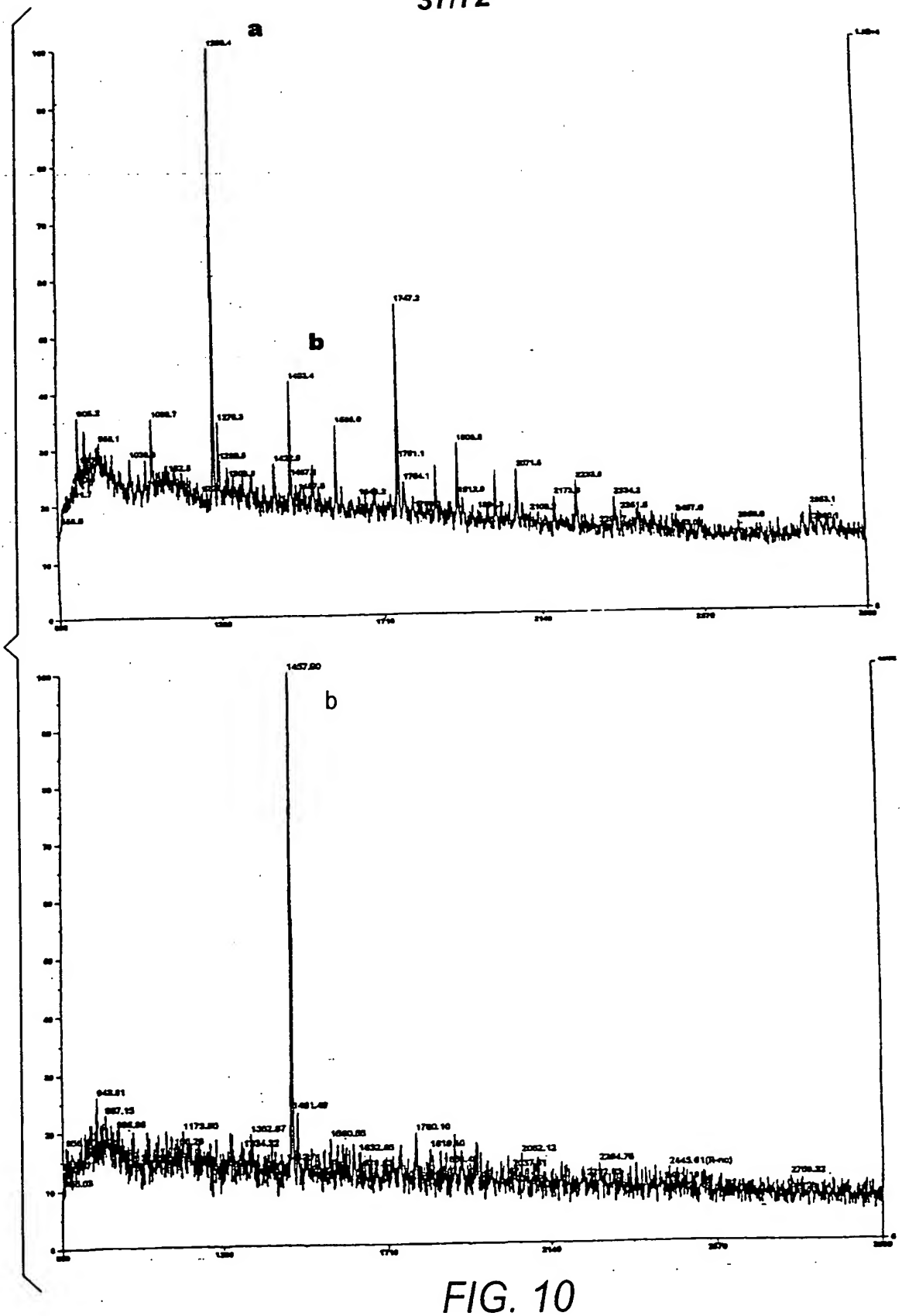


FIG. 10

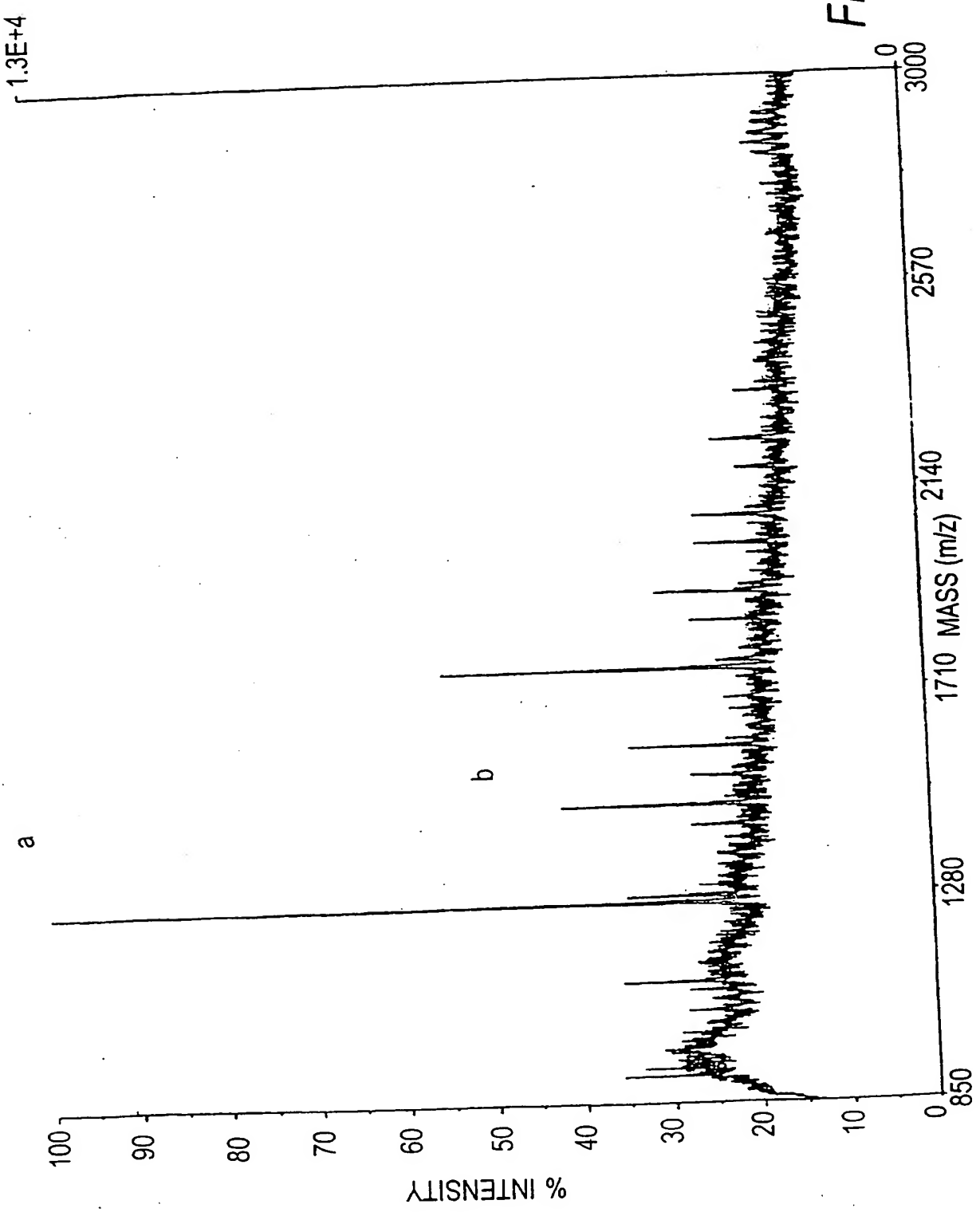

1.3E+4
a
b
% INTENSITY
100
90
80
70
60
50
40
30
20
10
0
850
1280
1710
2140
2570
3000
MASS (m/z)

FIG. 10A

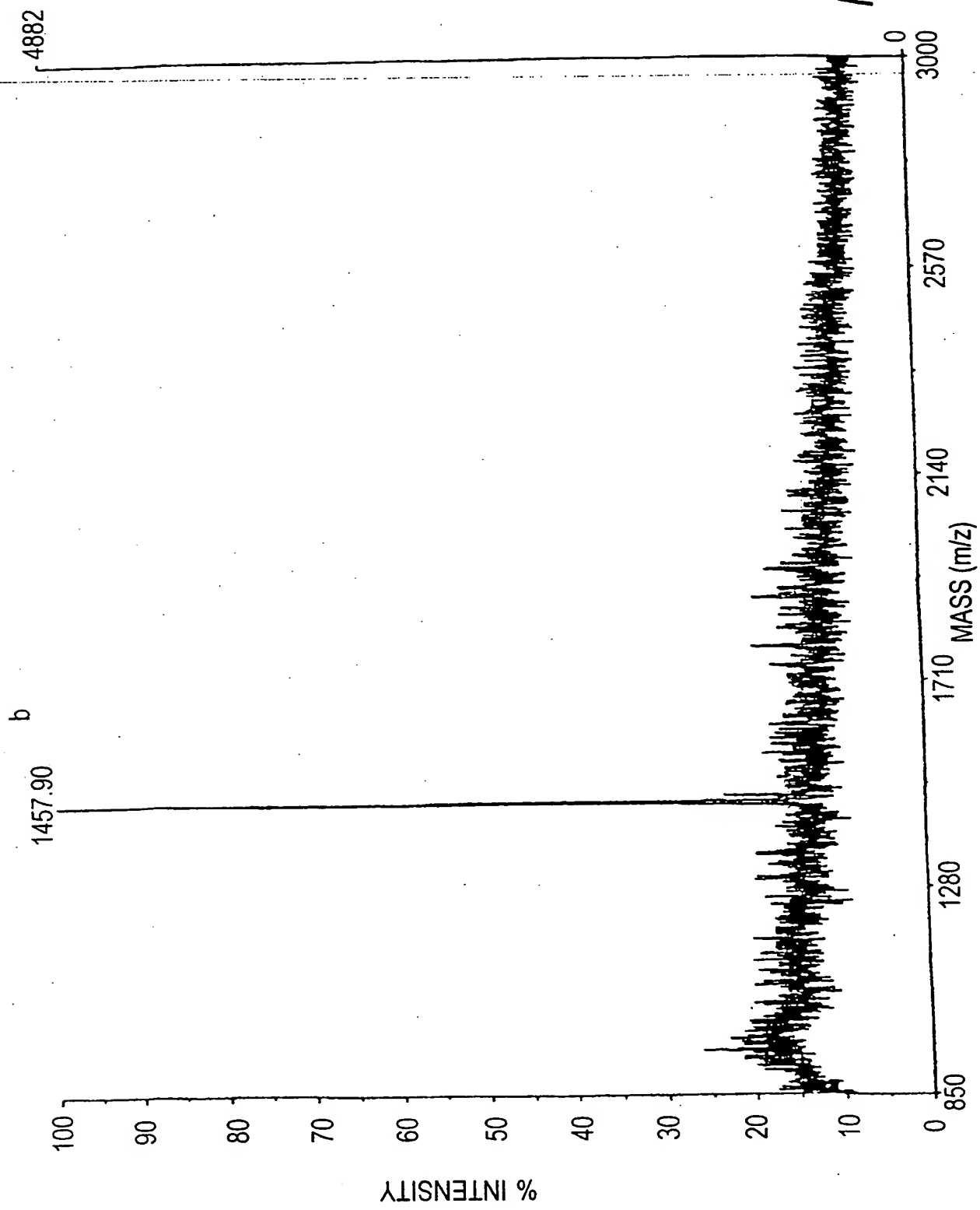

b
1457.90
4882
% INTENSITY
100
90
80
70
60
50
40
30
20
10
0
850
1280
1710
2140
2570
3000
0
MASS (m/z)

FIG. 10B

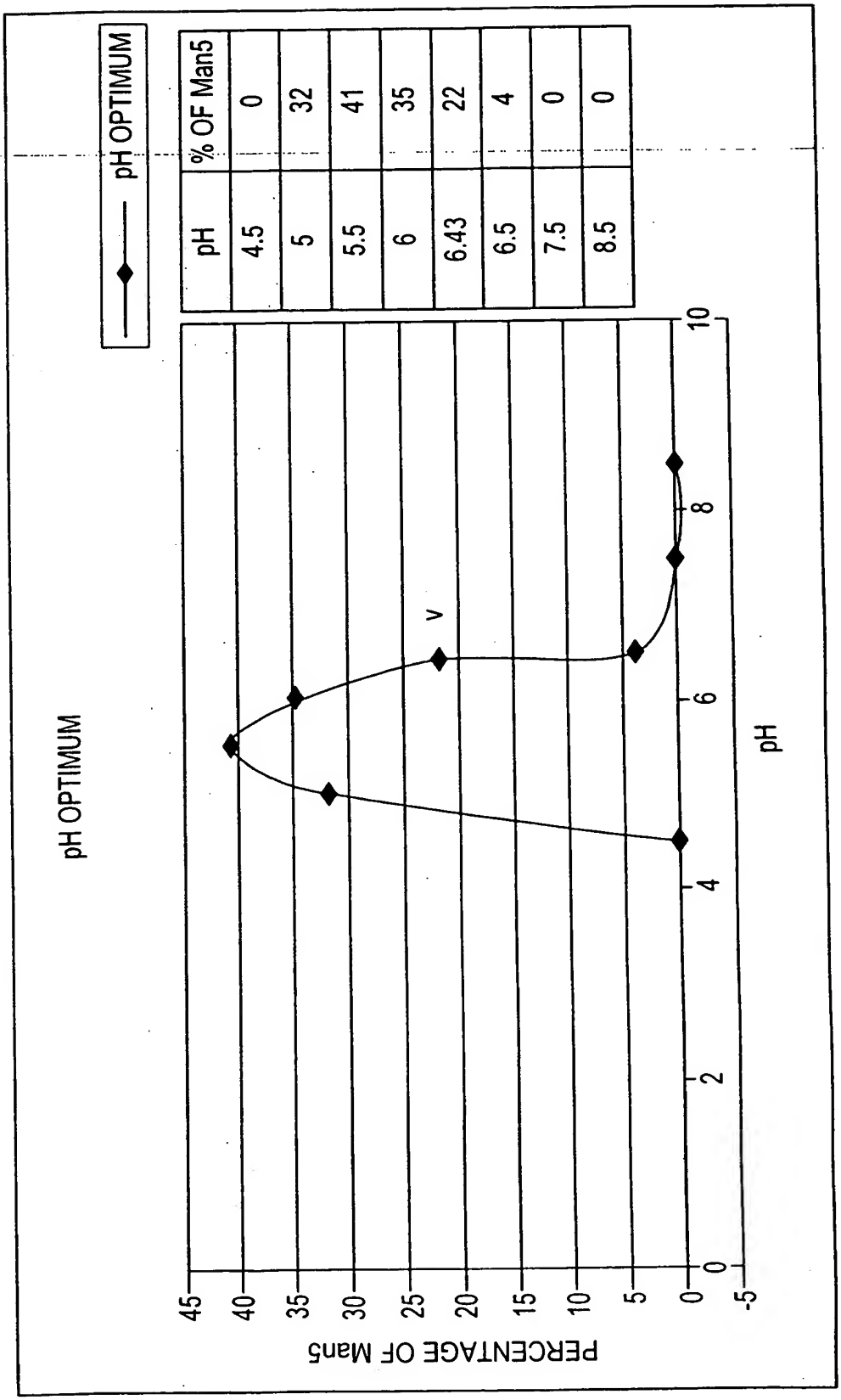

pH OPTIMUM
pH OPTIMUM
pH
PERCENTAGE OF Man5
45
40
35
30
25
20
15
10
5
0
-5
0
2
4
6
8
10
v
pH
% OF Man5
4.5
0
5
32
5.5
41
6
35
6.43
22
6.5
4
7.5
0
8.5
0

FIG. 11

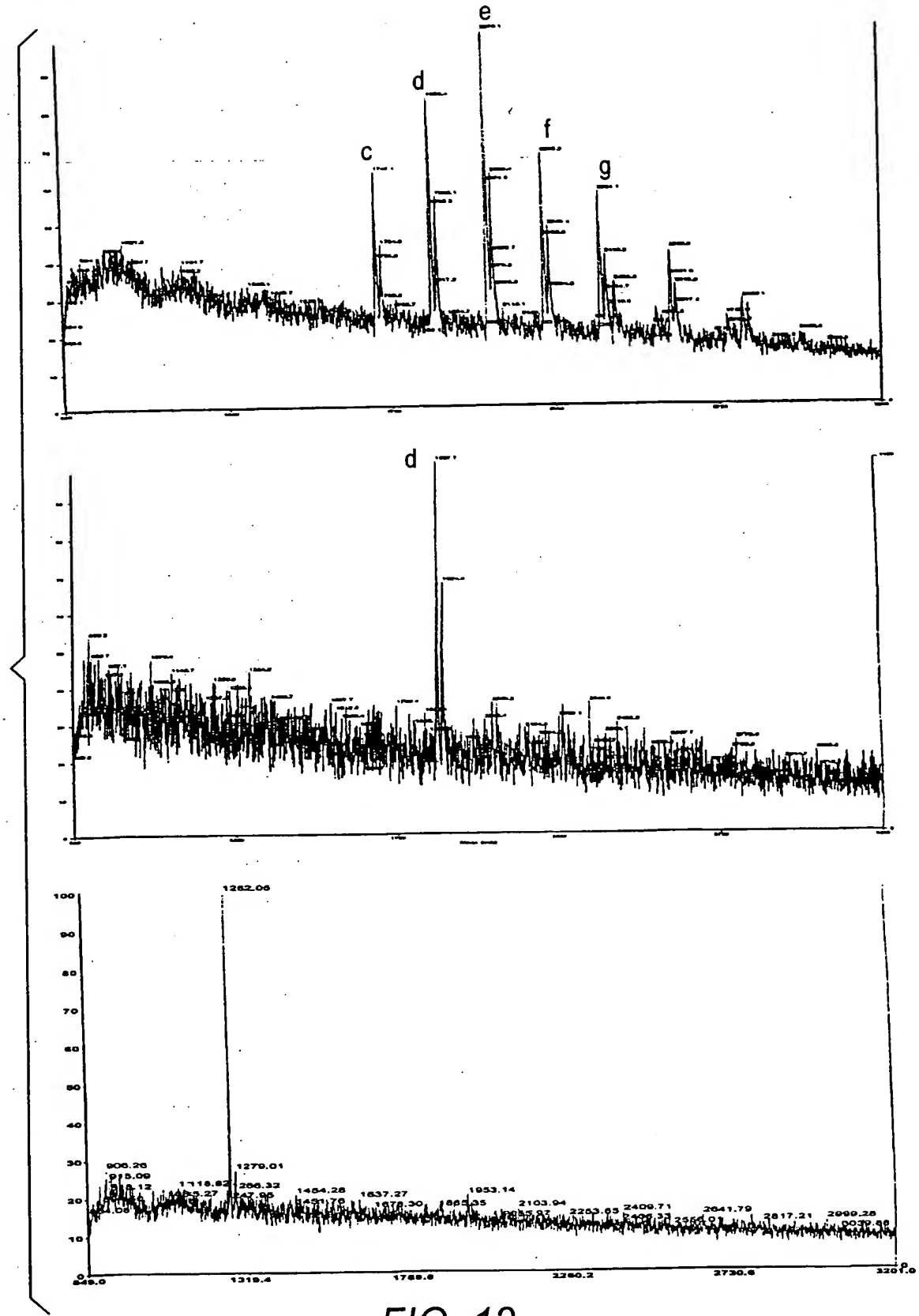

e
d
f
c
g
d
1262.06
100
90
80
70
60
50
40
30
20
10
0
906.26
915.09
1279.01
1953.14
1637.27
1464.28
2103.94
2400.71
2641.79
2817.21
2999.28
849.0
1319.4
1789.8
2260.2
2730.6
3201.0

FIG. 12

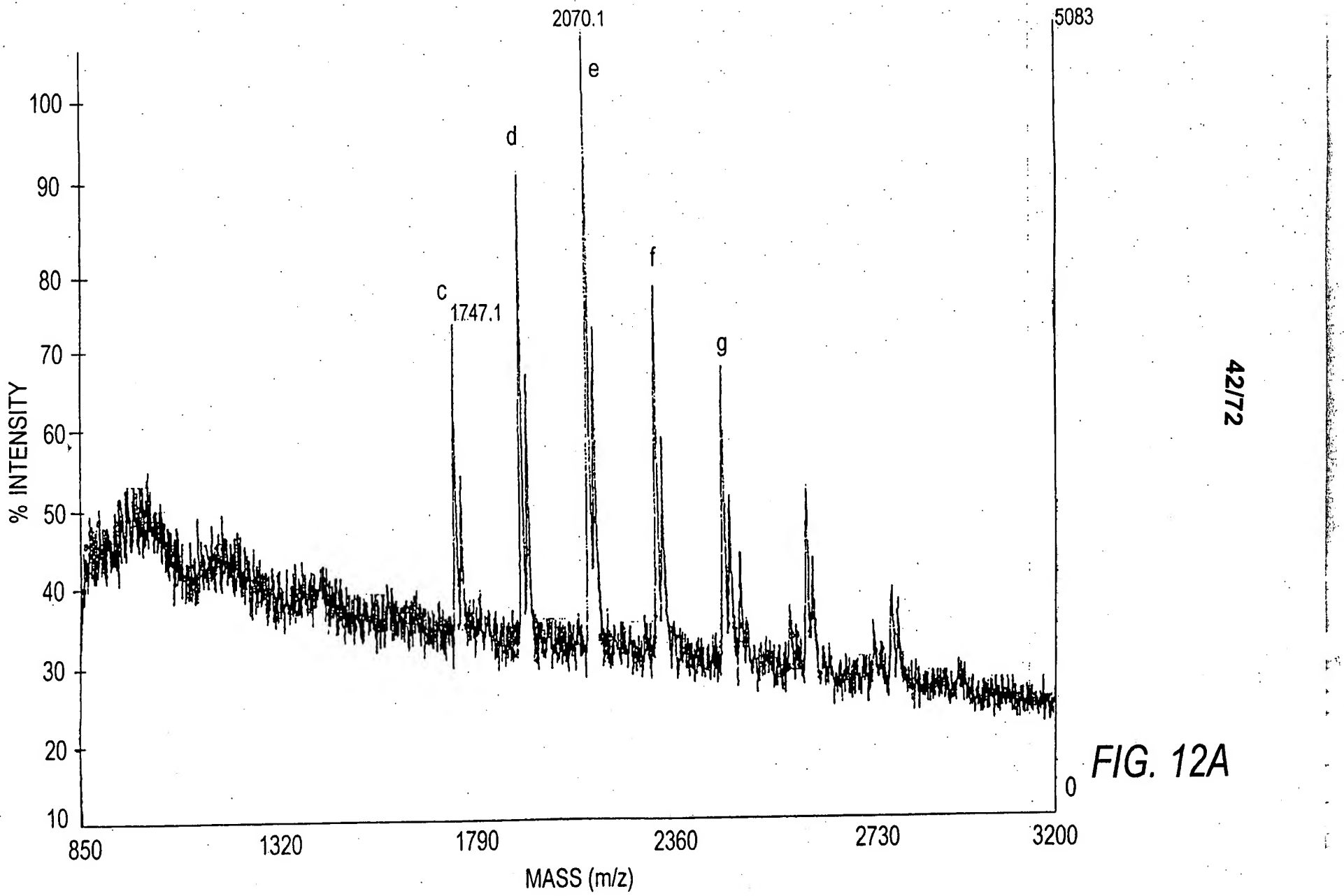

2070.1
5083
e
d
f
c
1747.1
g
100
90
80
70
60
50
40
30
20
10
% INTENSITY
0
850
1320
1790
2360
2730
3200
MASS (m/z)

FIG. 12A

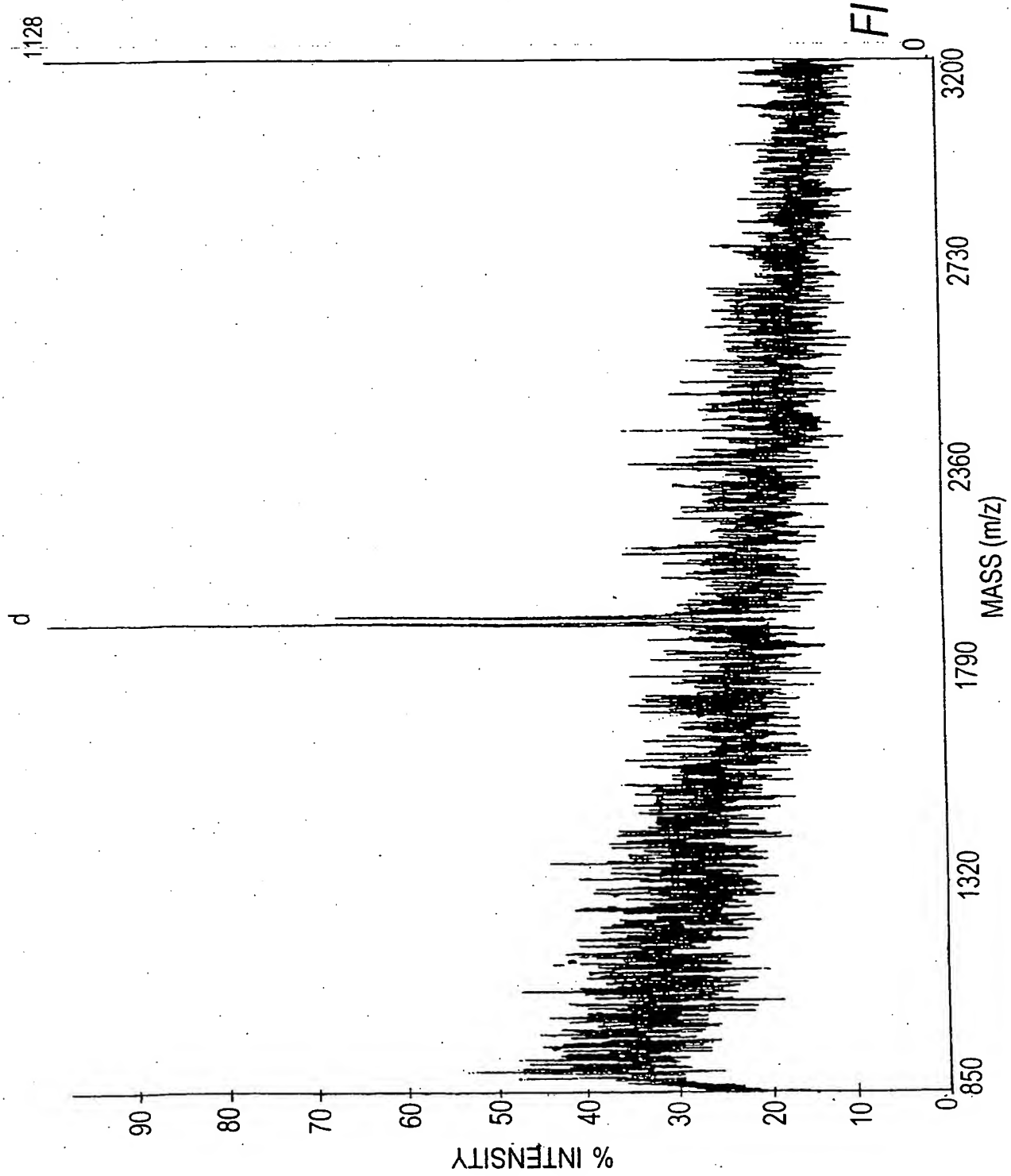

1128
d
% INTENSITY
90
80
70
60
50
40
30
20
10
0
850
1320
1790
2360
2730
3200
MASS (m/z)

FIG. 12B

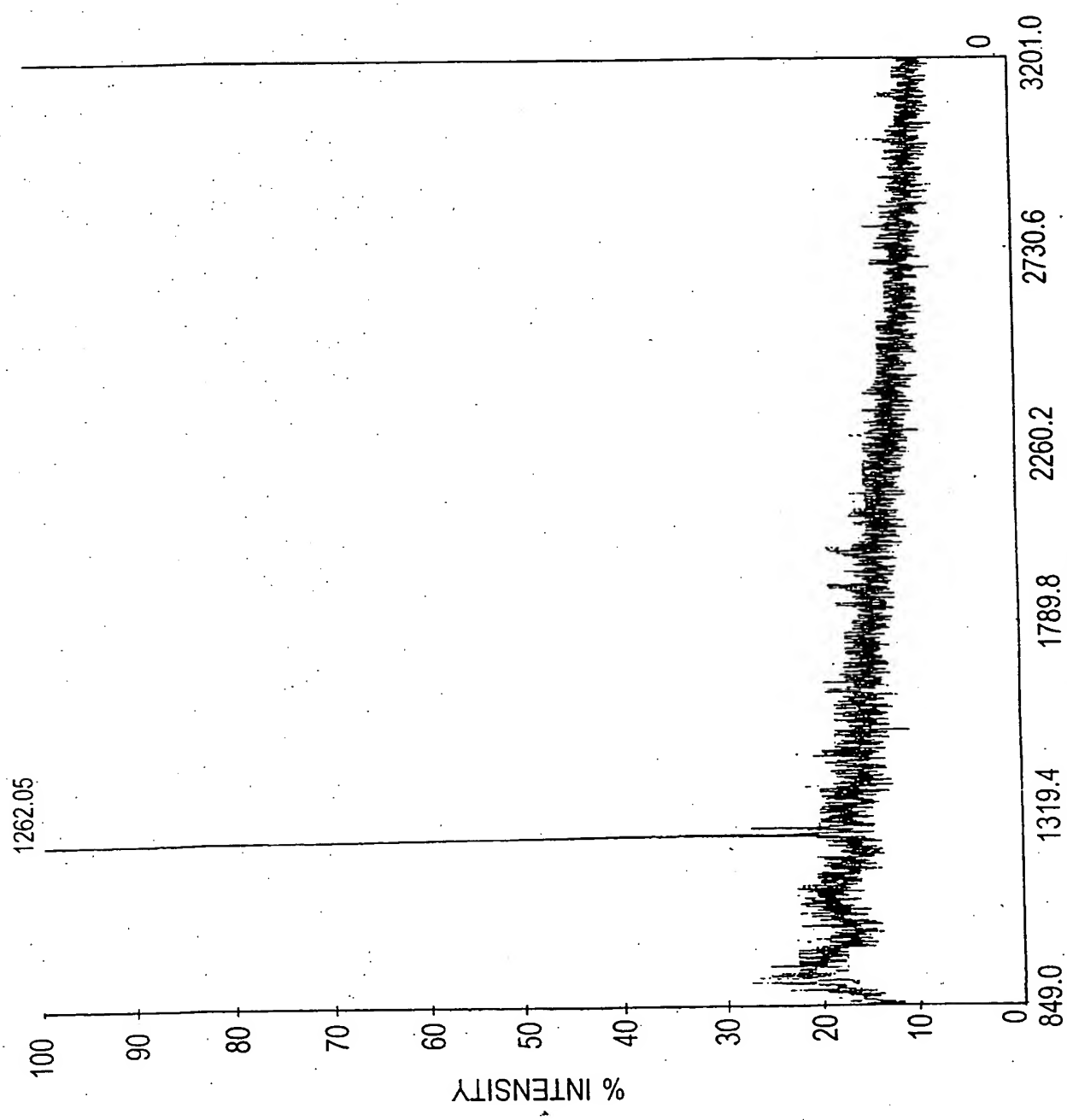

1262.05
100
90
80
70
60
50
40
30
20
10
0
% INTENSITY
849.0
1319.4
1789.8
2260.2
2730.6
3201.0
0
MASS (m/z)

FIG. 12C

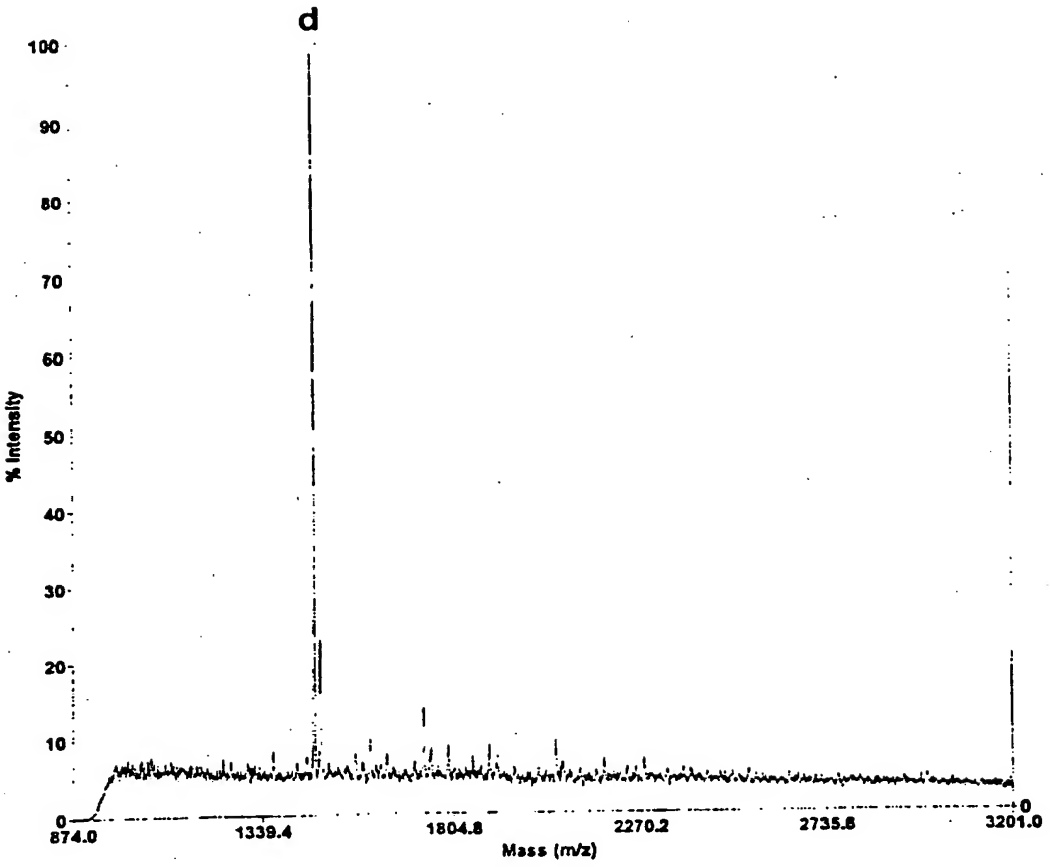

d
100
90
80
70
60
50
40
30
20
10
0
% Intensity
874.0
1339.4
1804.8
2270.2
2735.6
3201.0
0
Mass (m/z)

FIG. 13

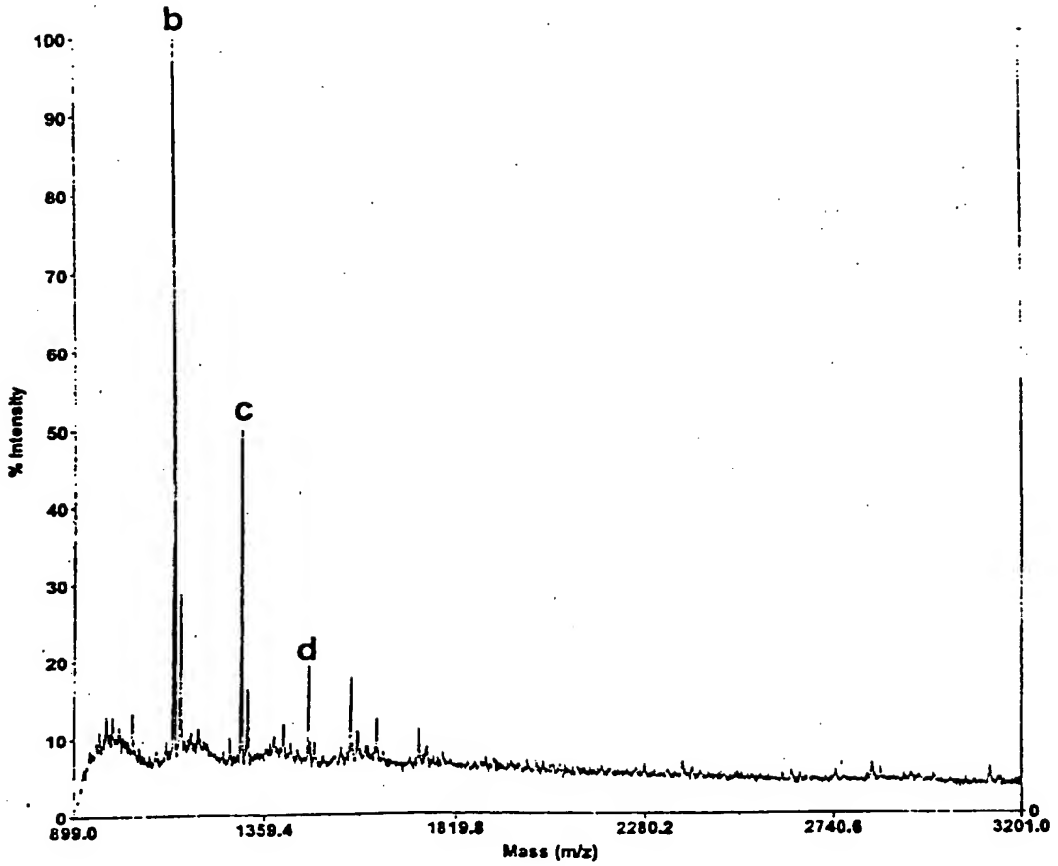

b
c
d
100
90
80
70
60
50
40
30
20
10
0
% Intensity
899.0
1359.4
1819.8
2280.2
2740.6
3201.0
Mass (m/z)

FIG. 14

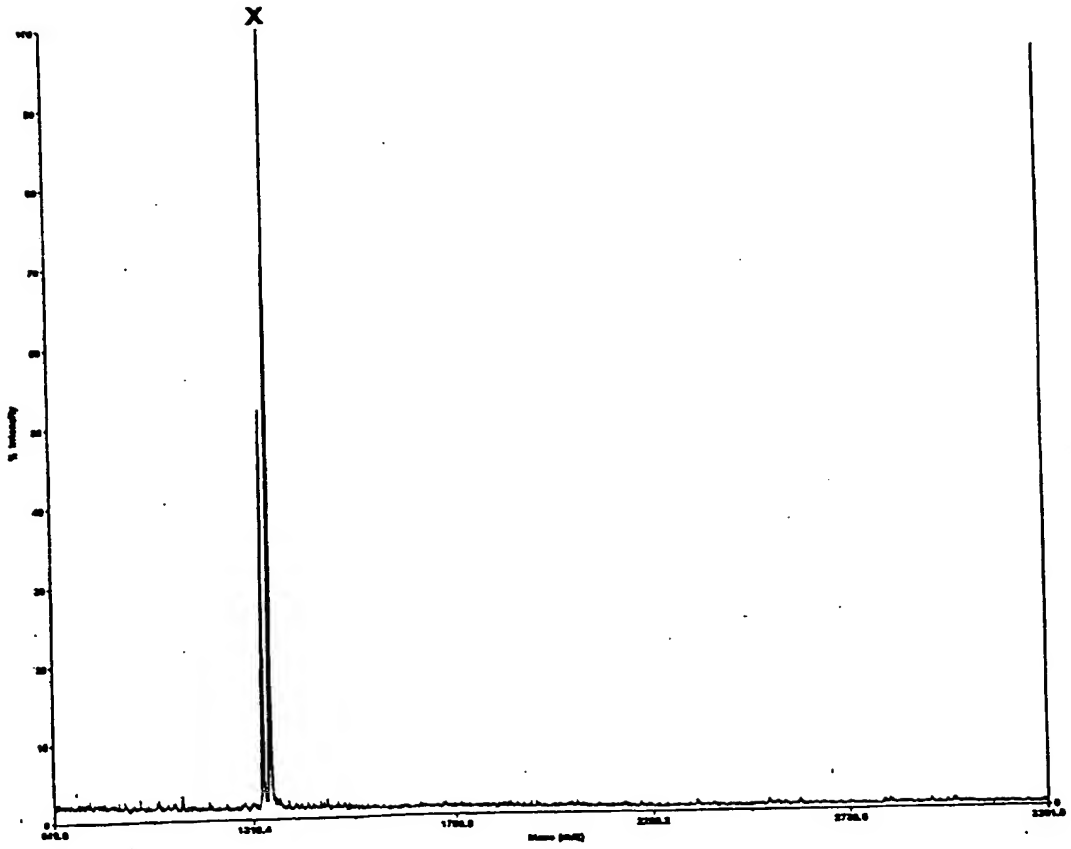


FIG. 15

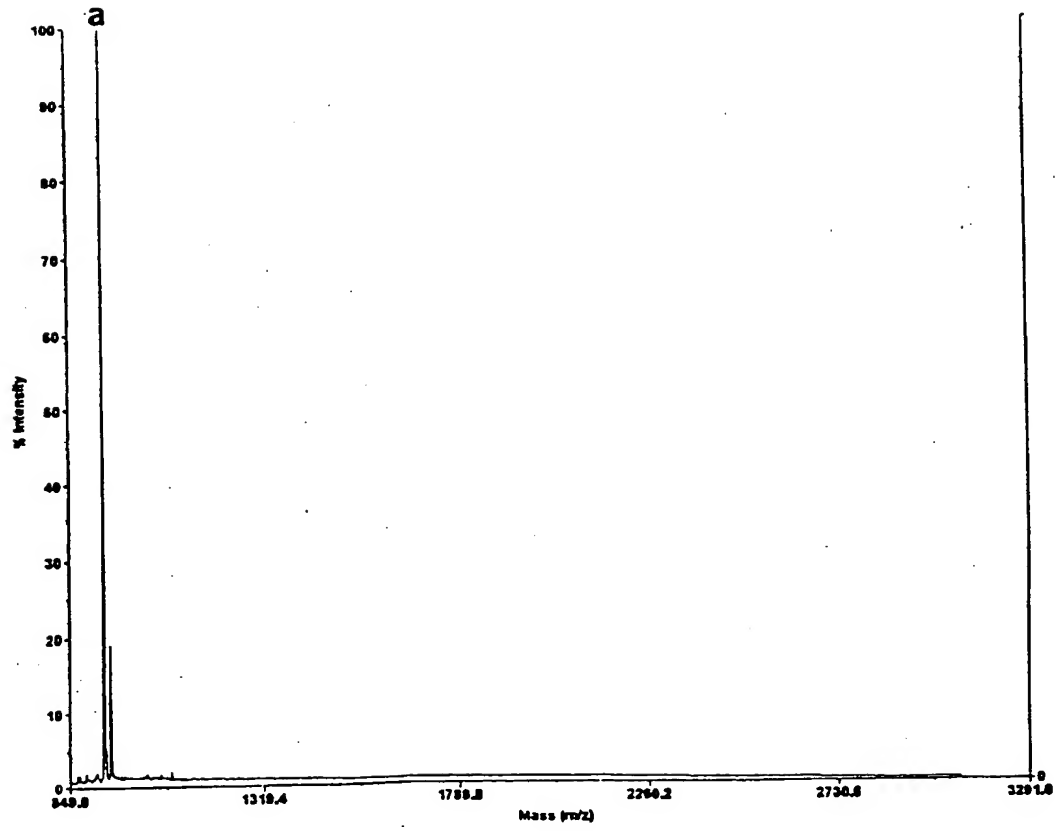
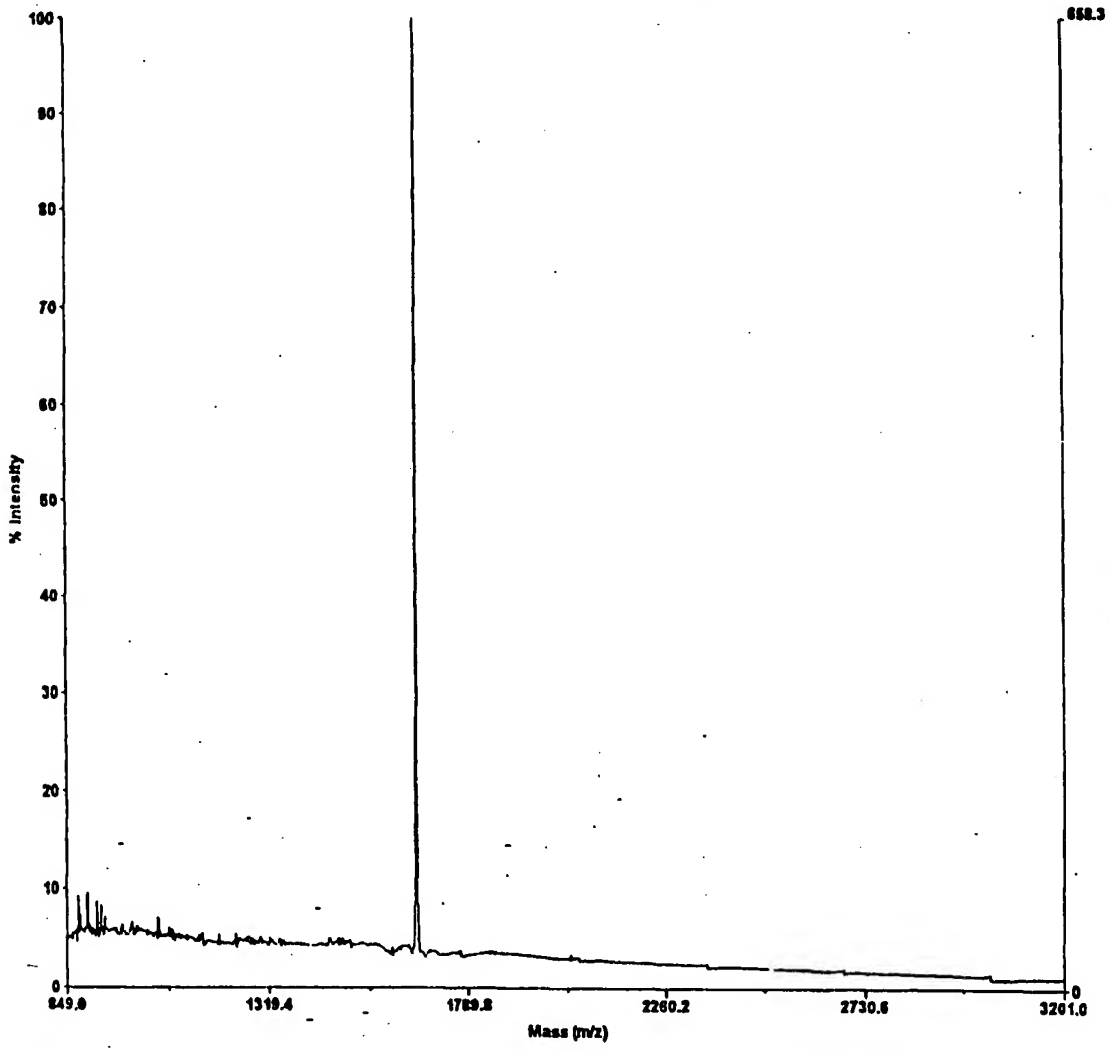

a
100
90
80
70
60
50
40
30
20
10
0
% Intensity
849.8
1319.4
1789.8
2260.2
2730.6
3201.0
Mass (m/z)

FIG. 16

FIG. 17

Applied Biosystems Voyager System 1246

V yager Spec #1=>BC=>NR(2.00)[BP = 1664.6, 658]



Mode of operation:	Linear
Extraction mode:	Delayed
Polarity:	Positive
658.3 Acquisition control:	Manual
Accelerating voltage:	20000 V
Grid voltage:	94%
Guide wire 0:	0.05%
Extraction delay time:	100 nsec
Acquisition mass range:	650 – 3200 Da
Number of laser shots:	100/spectrum
Laser intensity:	2713
Laser Rep Rate:	20.0 Hz
Calibration type:	Default
Calibration matrix:	2,5-Dihydroxybenzoic acid
Low mass gate:	800 Da
Digitizer start time:	18.582
Bin size:	2 nsec
Number of data points:	8676
Vertical scale:	500 mV
Vertical offset:	0%
Input bandwidth:	150 MHz
Sample well:	47
Plate ID:	100 WELL PLATE
Serial number:	1246
Instrument name:	Voyager-DE
Plate type filename:	C:\VOYAGER\100 well plate.pti
Lab name:	PE Biosystems
Absolute x-position:	31305.6
Absolute y-position:	28069.3
Relative x-position:	-761.913
Relative y-position:	1081.83
Shots in spectrum:	100
Source pressure:	4.393e-007
Mirror pressure:	0
TC2 pressure:	0.004253
TIS gate width:	30
TIS flight length:	940

Milestone IV gal

Acquired: 10:12:00, June 13, 2003

Printed: 08:41, June 16, 2003

D:\GLYCO-FI DATA\Huijuan Data\Other samples\June 2003\HL 6-13-03 Gal transfer\6-2-03 SH MIV GN2M3 + GalT 5ul_0001.dat

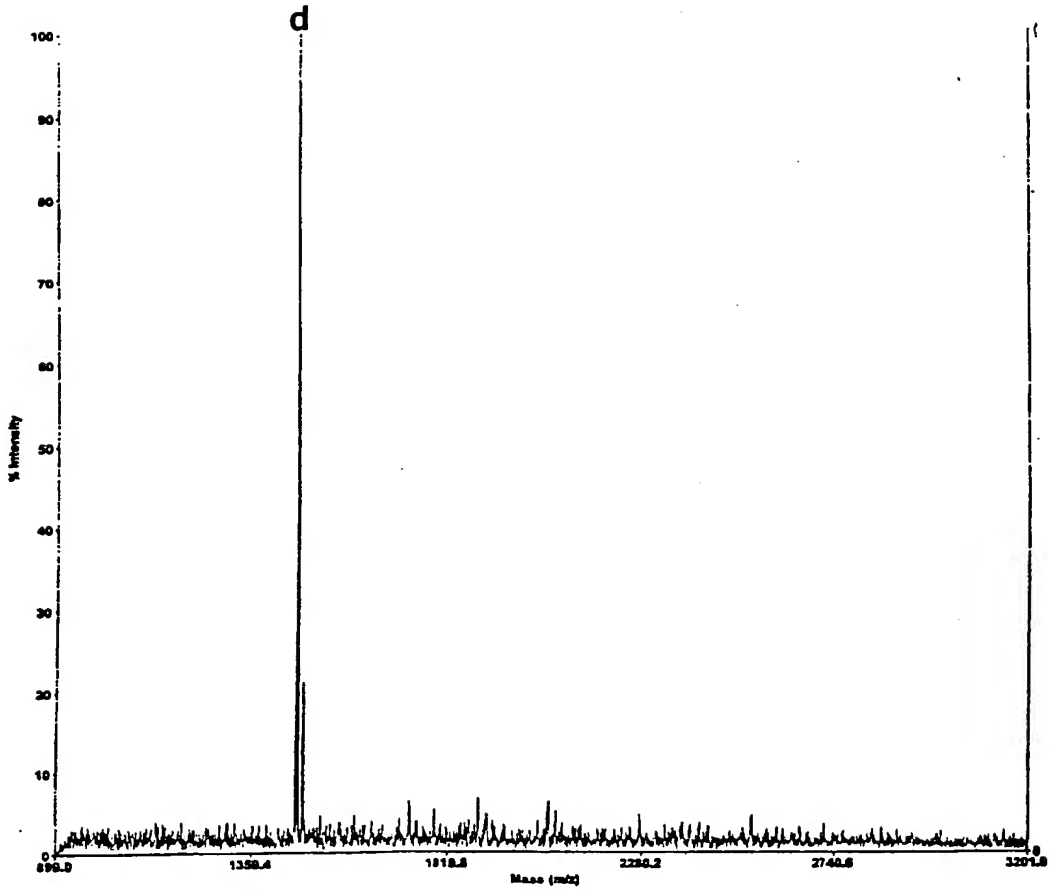

d
100
90
80
70
60
50
40
30
20
10
0
% Intensity
899.9
1359.4
1819.8
2280.2
2740.6
3201.0
Mass (m/z)

FIG. 18

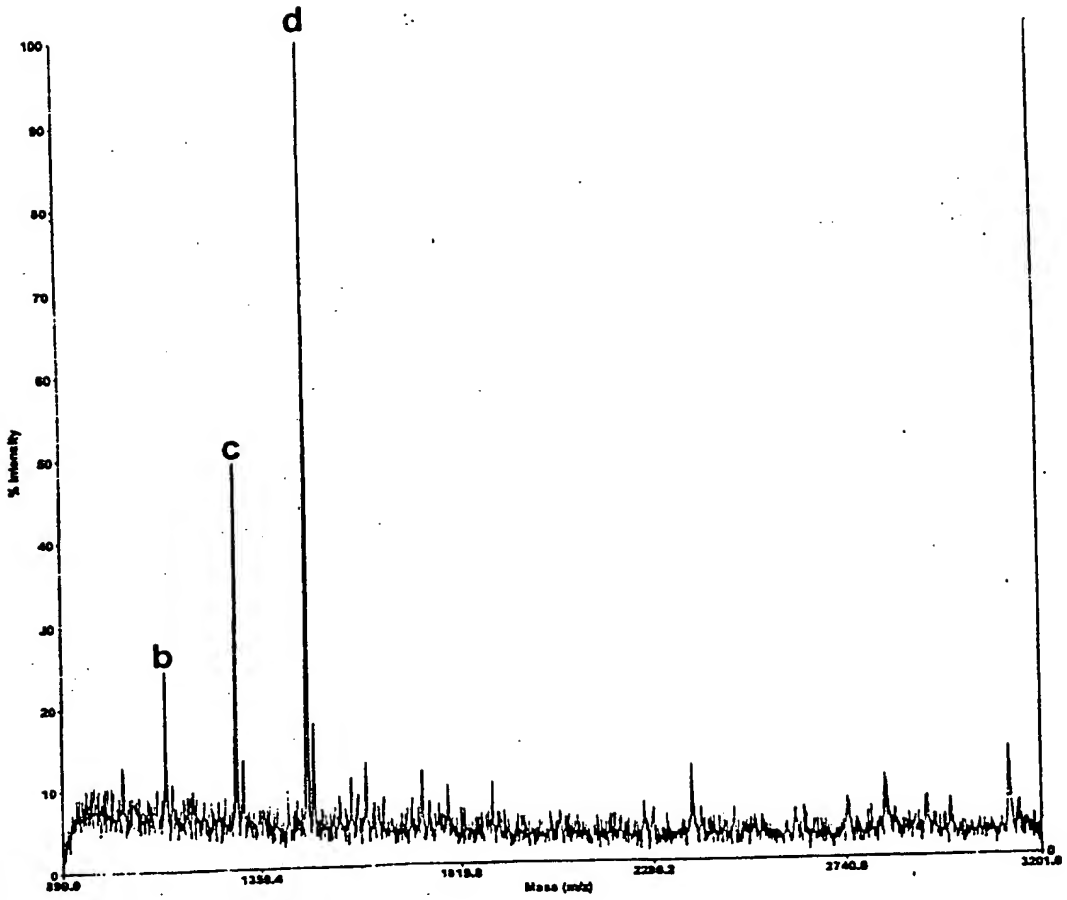

d
c
b
100
90
80
70
60
50
40
30
20
10
0
% Intensity
890.8
1338.4
1819.8
2298.2
2740.8
3201.8
Mass (m/z)

FIG. 19

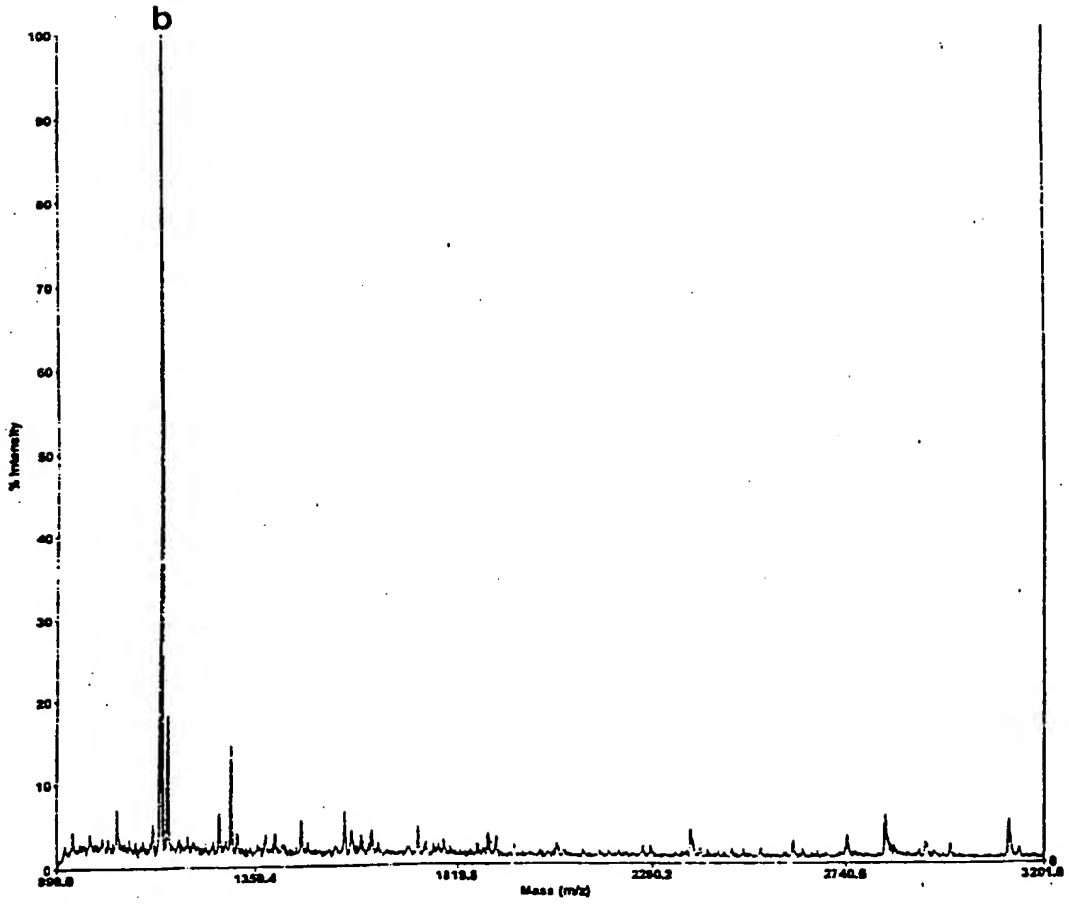

b
100
90
80
70
60
50
40
30
20
10
0
% Intensity
898.8
1359.4
1819.8
2280.2
2740.6
3201.0
Mass (m/z)

FIG. 20

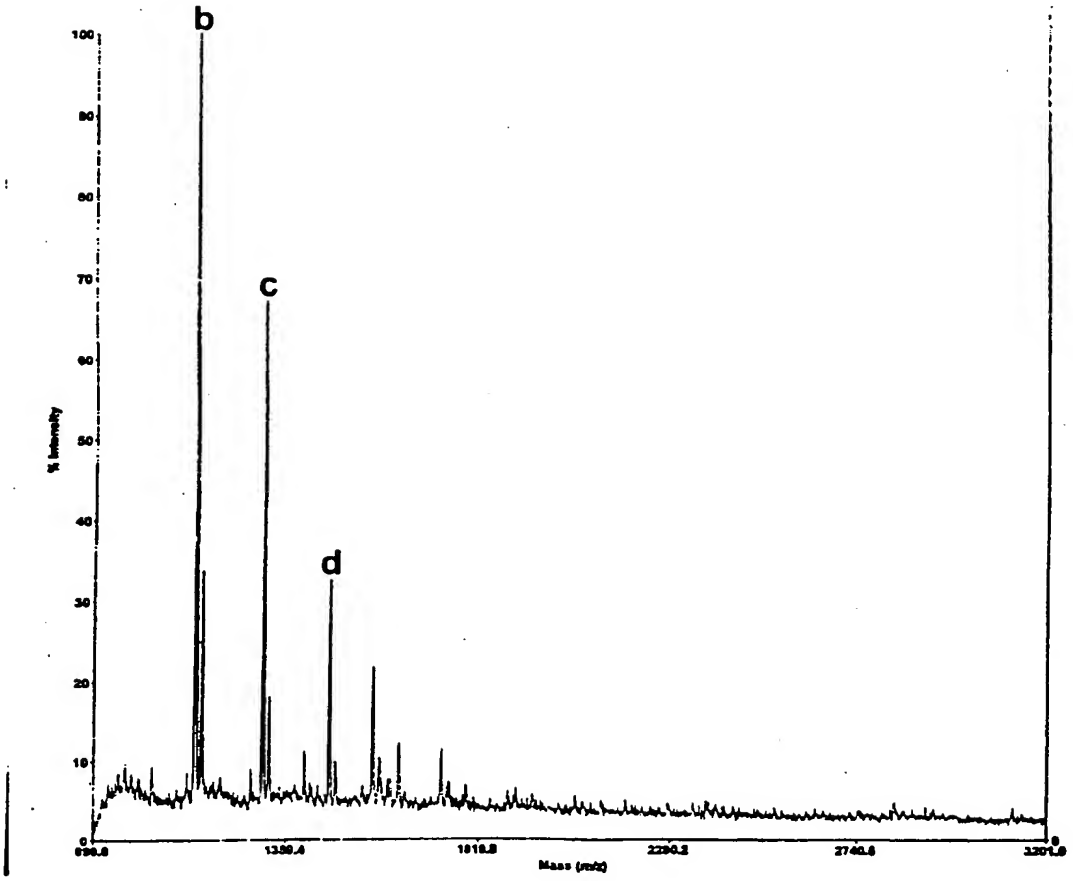


FIG. 21

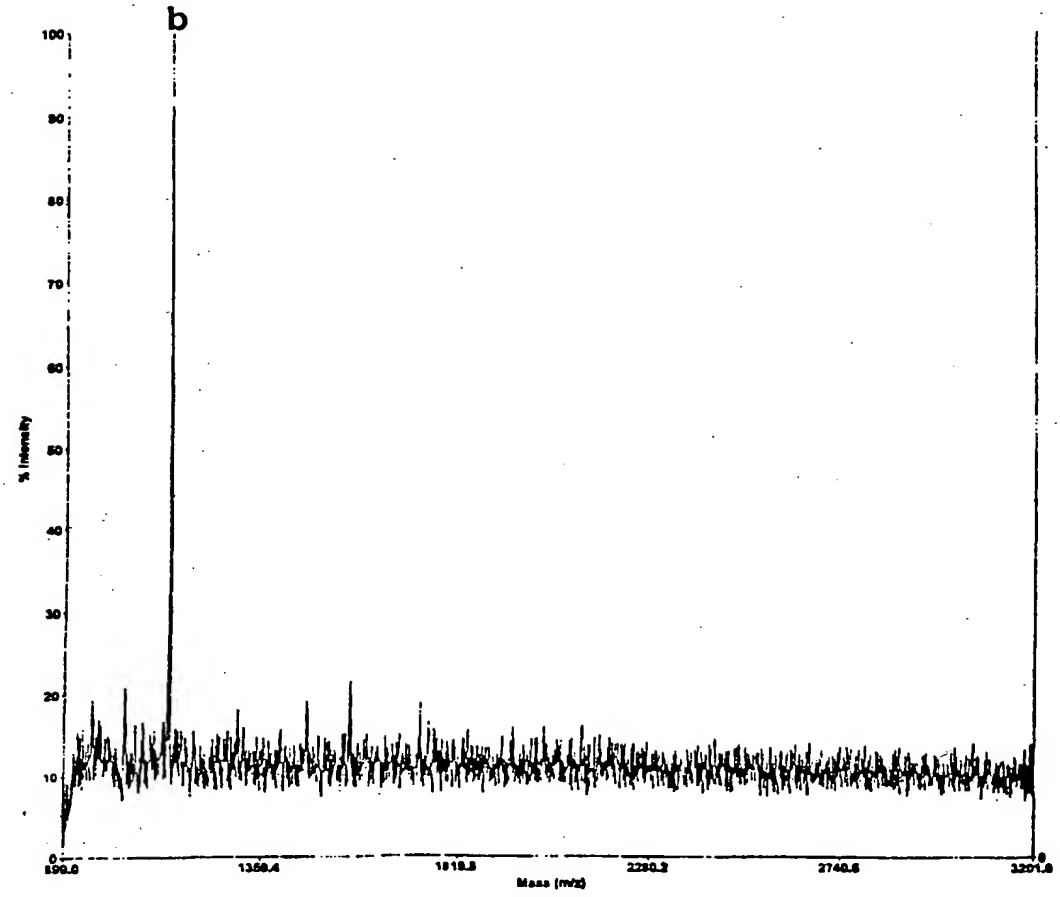
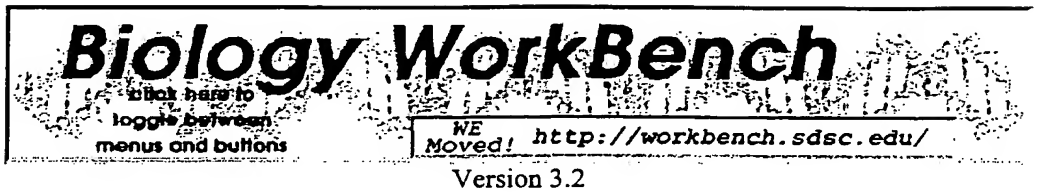

b
100
90
80
70
60
50
40
30
20
10
0
% Intensity
898.0
1358.4
1818.8
2280.2
2740.6
3201.0
Mass (m/z)

FIG. 22



Version 3.2

BOXSHADE

Color-Coded Plots of Pre-Aligned Sequences

Selected Sequence(s)

- Droso MannII (X77652),

C.elegans MannII,
rMannII (XM_218816.1),
hMannIIx D55649,
Mouse MannII (X61172),
human MannII (U31520),
CionaMannII (AK116684),
ArabMannII,
Insect ManIII,
hLyso MannII,
hCyto MannII (NM_006715)

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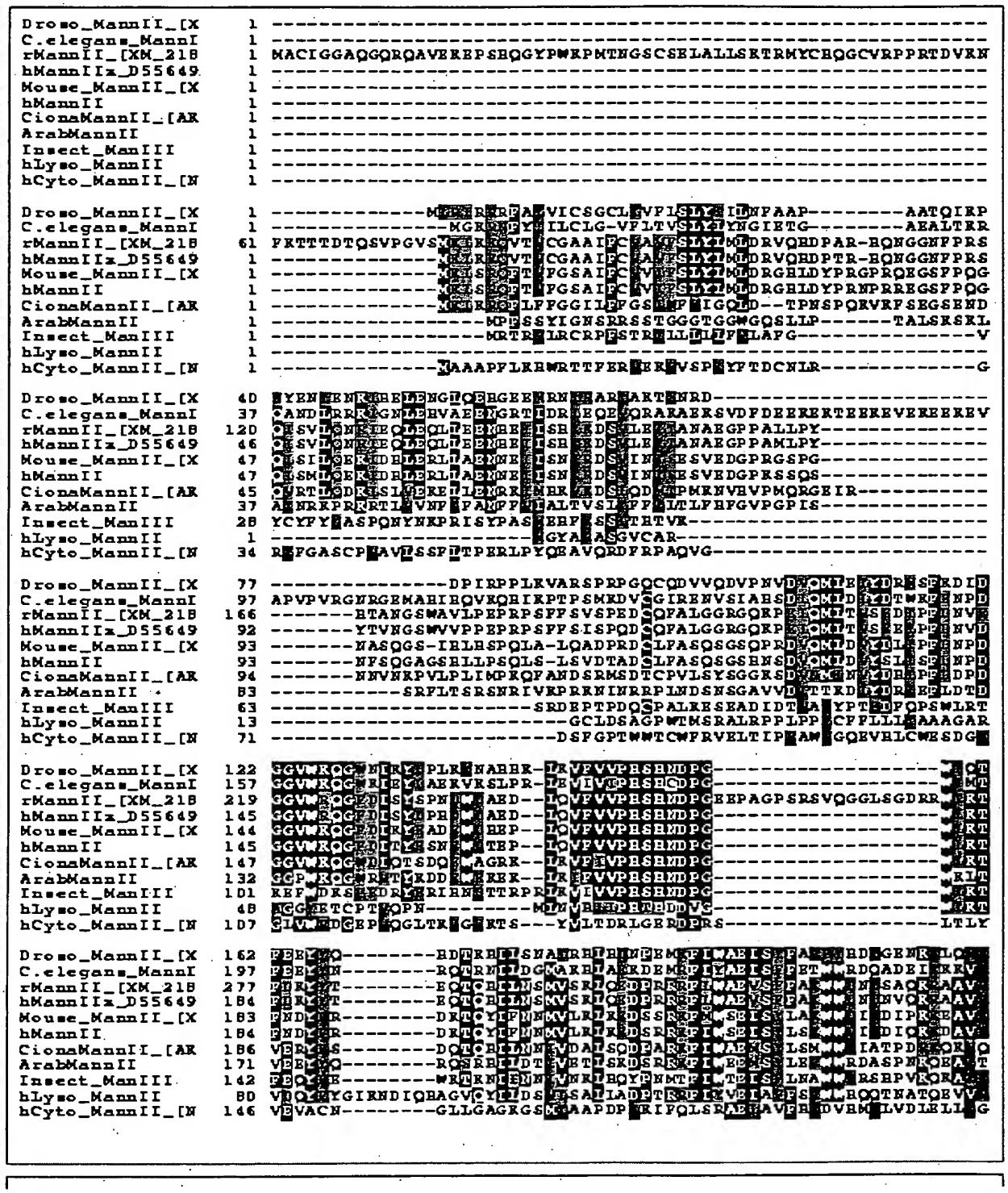
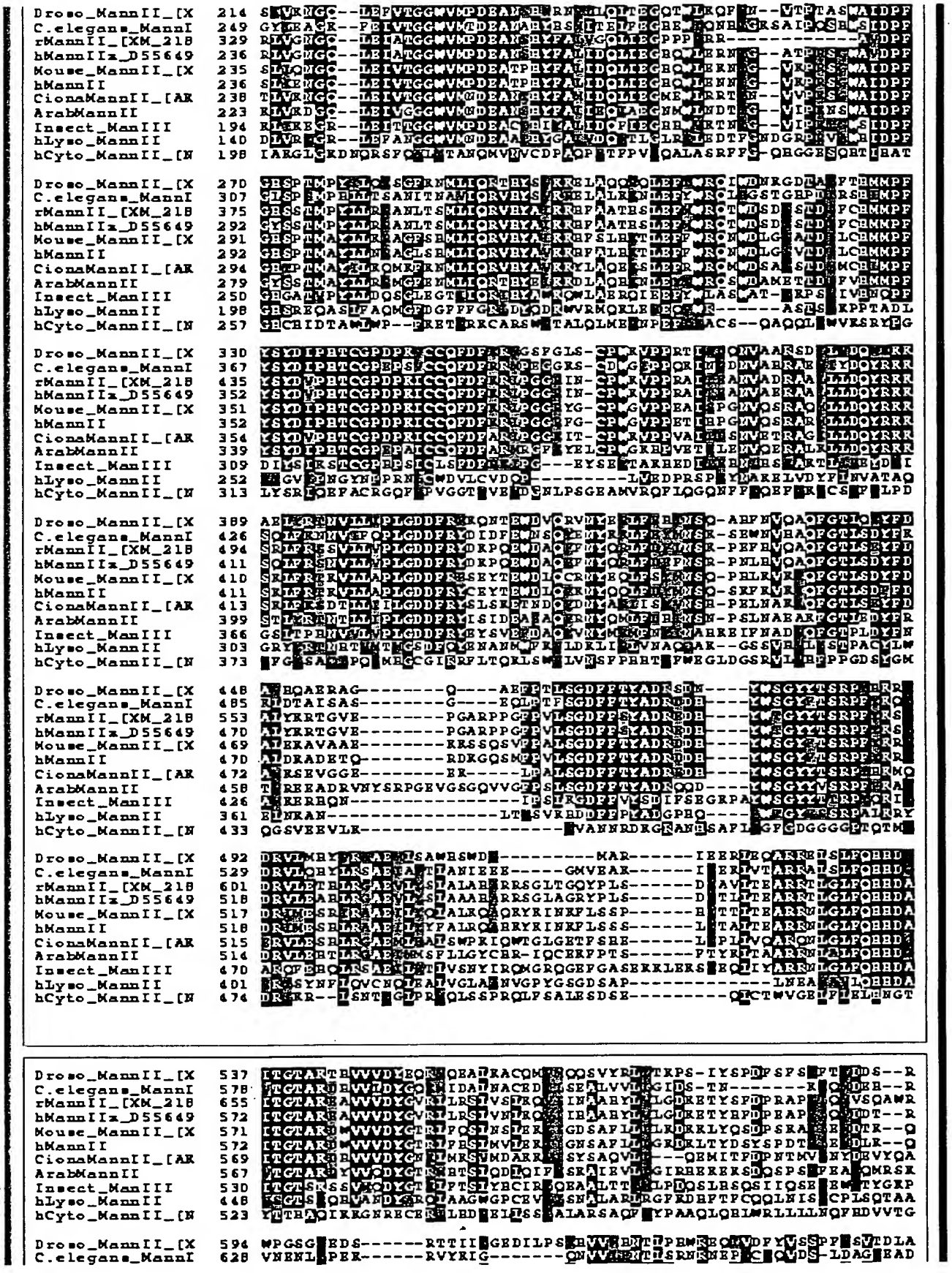
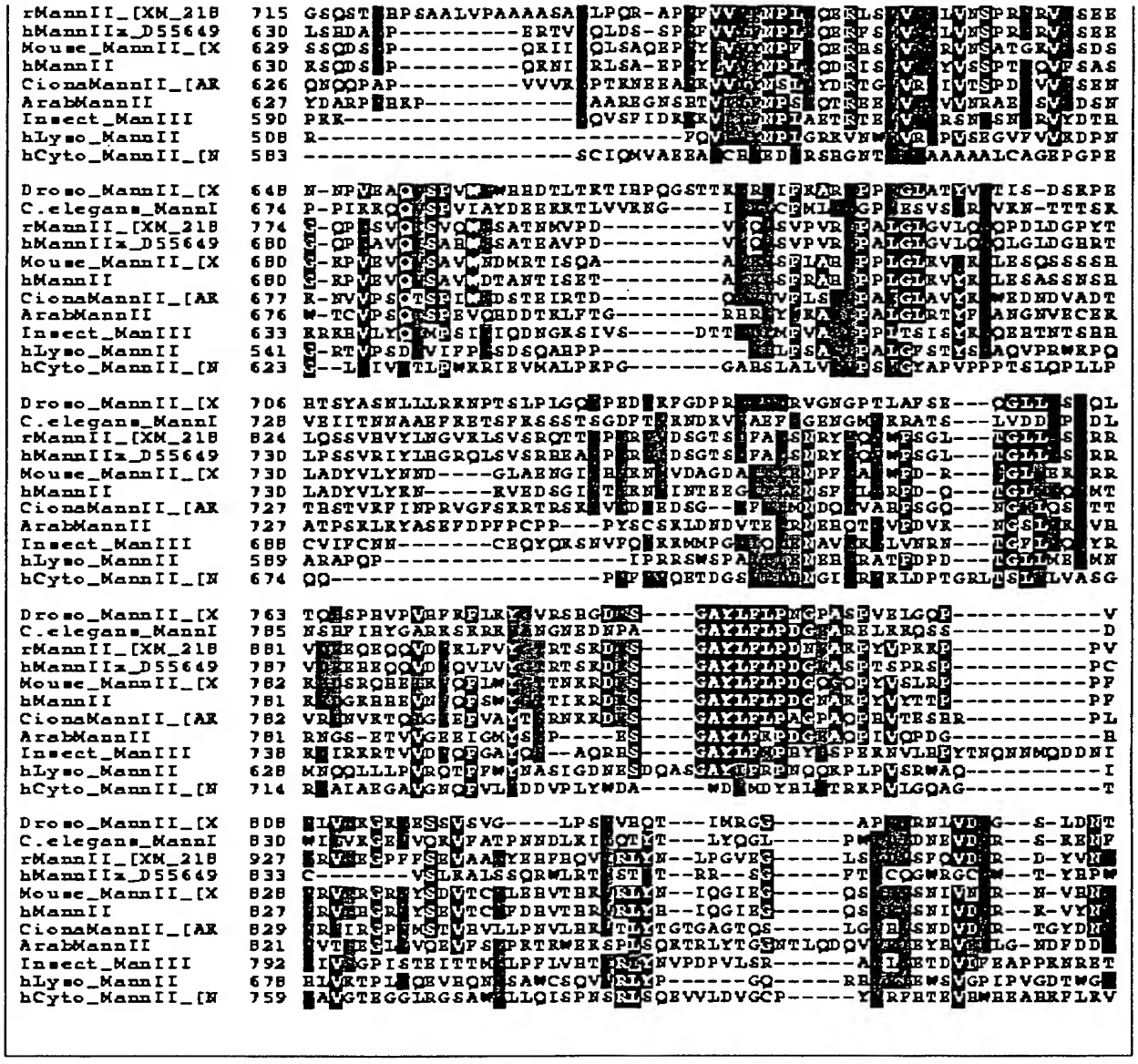
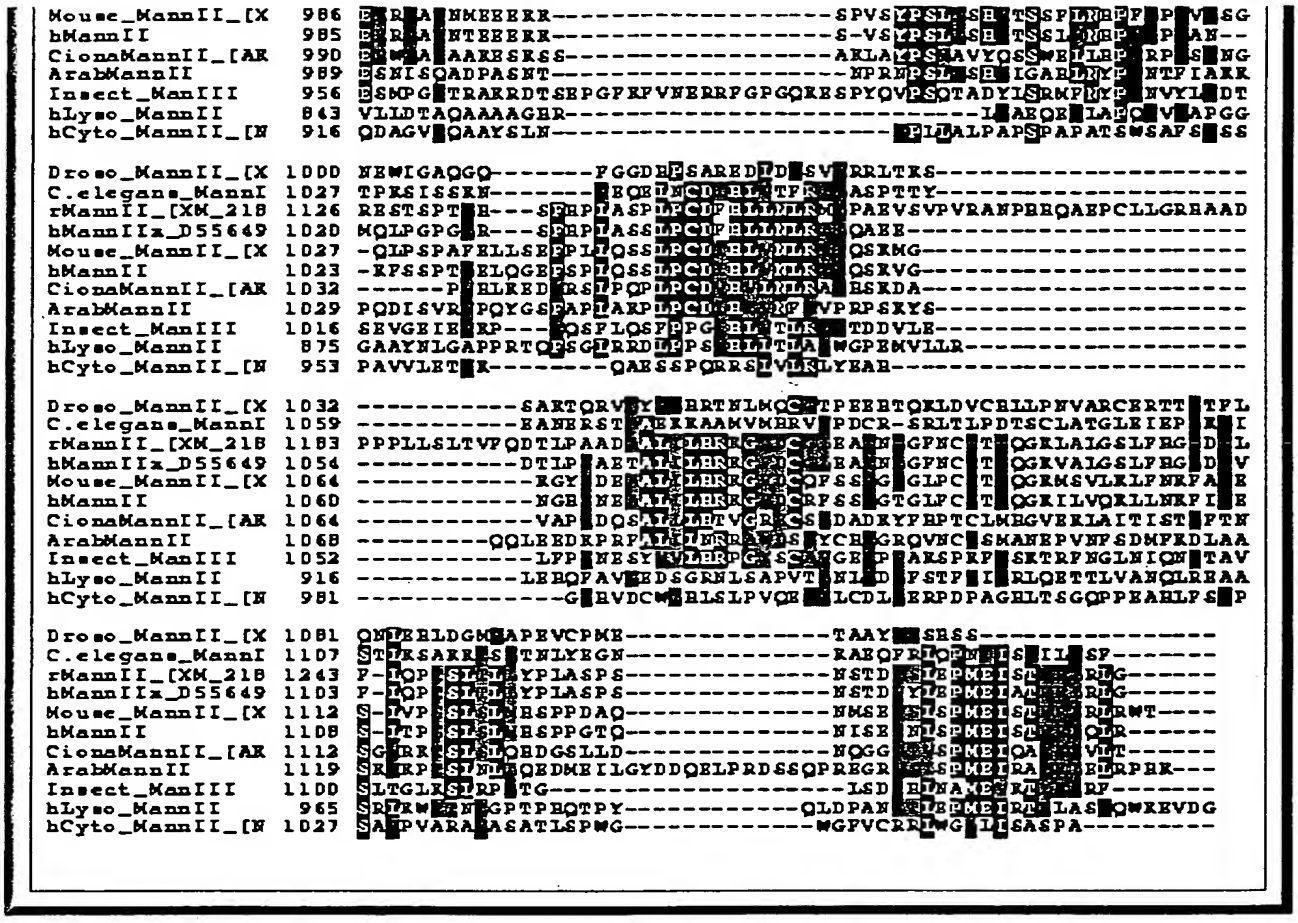
FIG. 23

Download a PostScript version of the output






rMannII_[XM_218 715
hMannIIx_D55649 630
Mouse_MannII_[X 629
hMannII 630
CionaMannII_[AR 626
ArabMannII 627
Insect_ManIII 590
hLyso_MannII 508
hCyto_MannII_[N 583
Droso_MannII_[X 648
C.elegans_MannI 674
rMannII_[XM_218 774
hMannIIx_D55649 680
Mouse_MannII_[X 680
hMannII 680
CionaMannII_[AR 677
ArabMannII 676
Insect_ManIII 633
hLyso_MannII 541
hCyto_MannII_[N 623
Droso_MannII_[X 706
C.elegans_MannI 728
rMannII_[XM_218 826
hMannIIx_D55649 730
Mouse_MannII_[X 730
hMannII 730
CionaMannII_[AR 727
ArabMannII 727
Insect_ManIII 688
hLyso_MannII 589
hCyto_MannII_[N 674
Droso_MannII_[X 763
C.elegans_MannI 785
rMannII_[XM_218 881
hMannIIx_D55649 787
Mouse_MannII_[X 782
hMannII 781
CionaMannII_[AR 782
ArabMannII 781
Insect_ManIII 738
hLyso_MannII 628
hCyto_MannII_[N 714
Droso_MannII_[X 808
C.elegans_MannI 830
rMannII_[XM_218 927
hMannIIx_D55649 833
Mouse_MannII_[X 828
hMannII 827
CionaMannII_[AR 829
ArabMannII 821
Insect_ManIII 792
hLyso_MannII 678
hCyto_MannII_[N 759
Droso_MannII_[X 852
C.elegans_MannI 879
rMannII_[XM_218 977
hMannIIx_D55649 874
Mouse_MannII_[X 878
hMannII 877
CionaMannII_[AR 882
ArabMannII 880
Insect_ManIII 846
hLyso_MannII 727
hCyto_MannII_[N 814
Droso_MannII_[X 902
C.elegans_MannI 929
rMannII_[XM_218 1027
hMannIIx_D55649 922
Mouse_MannII_[X 928
hMannII 927
CionaMannII_[AR 932
ArabMannII 930
Insect_ManIII 898
hLyso_MannII 785
hCyto_MannII_[N 858
Droso_MannII_[X 960
C.elegans_MannI 987
rMannII_[XM_218 1085
hMannIIx_D55649 980



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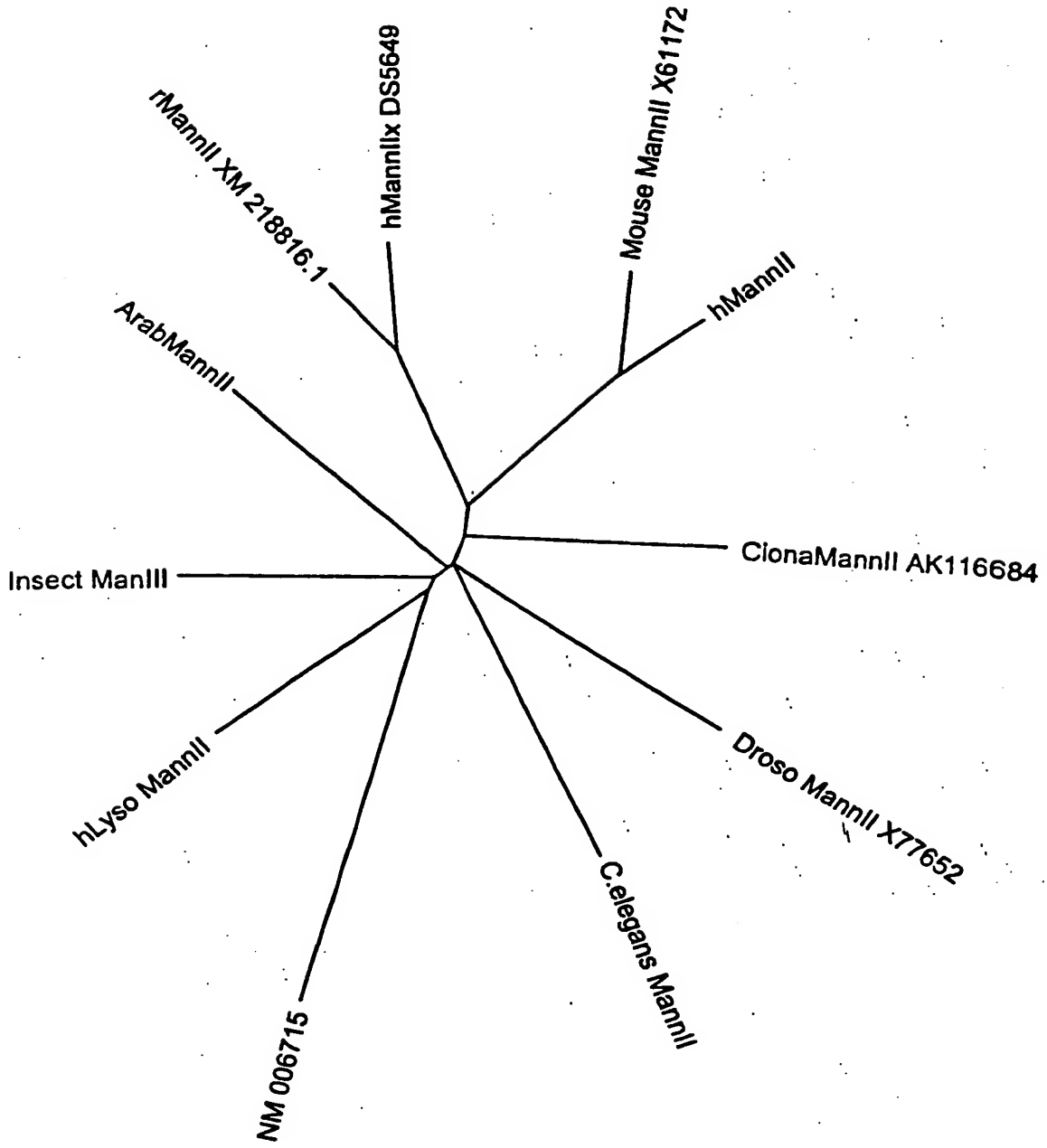
Citation

Algorithm Citation:
Not given, but presumably Kay Hofmann and Michael D. Baron.
Program Citation:
Boxshade version 3.3.1, by Kay Hofmann and Michael D. Baron.

FIG. 24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hMannIIx DS5649
Mouse MannII X61172
hMannII
ArabMannII
ClonaMannII AK116684
Insect ManIII
hLyso MannII
Droso MannII X77652
C.elegans MannII
NM 006715

FIG. 25

Arabidopsis thaliana Mannosidase II (NM_121499)

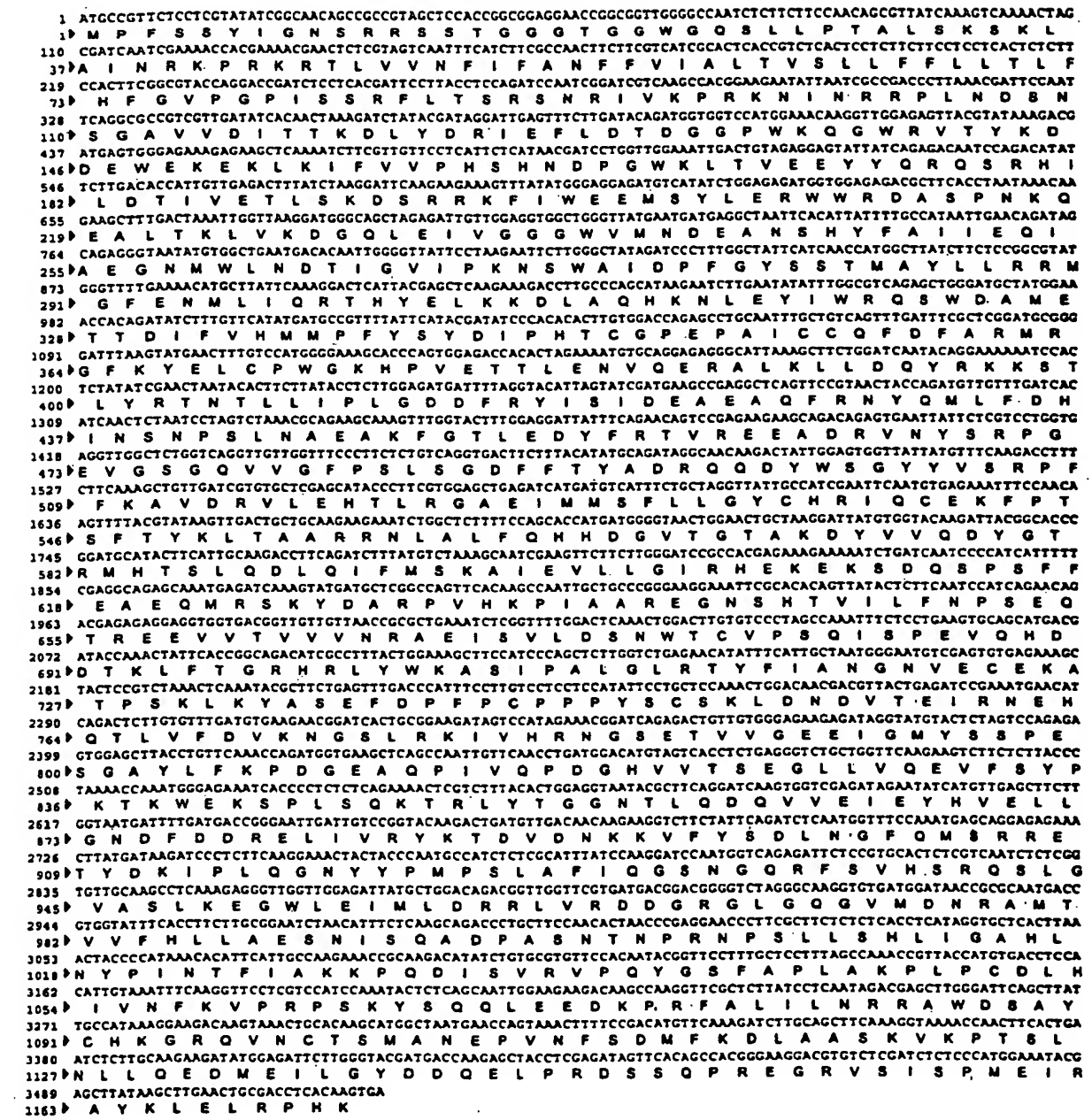

FIG. 26

C. elegans Mannosidase II (NM_073594)

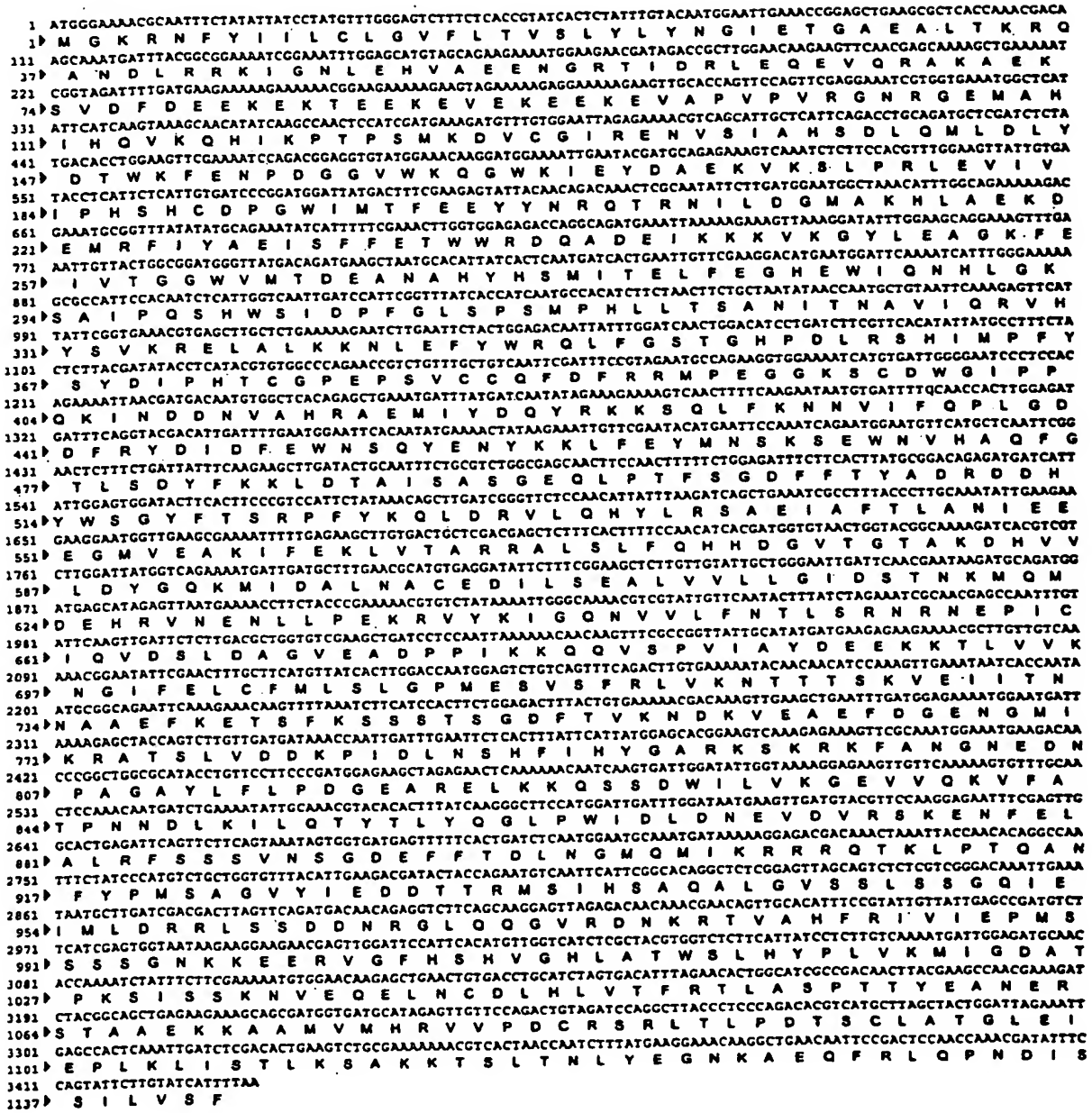

FIG. 27

Ciona intestinalis mannosidase II (AK116684)

```
   1 ATGAAGCTCAAACGCCAGTTCTTATTCTTTGGTGGAATTCTGTTCTTCGGGAGTATCTGGTTTATGATAGGTCAACTTGACACTCCTAATTCGCCACAGAAAGTCAAAT
   1 M K L K R Q F L F F G G I L F F G S I W F M I G Q L D T P N S P Q K V K
 110 TCTCGGAAGGCAGTGAAAATGACCAAGTTCGAACCCTTCAAGACAAACTTAGTCTGGTCGAAAAAGAATTGTTAGAAAATCGTAAAATAATGCACAAGGTGAAAGATAG
  37 F S E G S E N D Q V R T L Q D K L S L V E K E L L E N R K I M H K V K D S
 219 TCTACAGGATATGACACCCATGAAAAATGTTCATGTGCCTATGCAGCGCGGAGAAATAAGAAACAACGTCAATAAACCTGTGCTACCACTTATAATGCCCAAGCAATTT
  73 L Q D M T P M K N V H V P M Q R G E I R N N V N K P V L P L I M P K Q F
 328 GCGAATGACTCCCGAATGAGTGACACGTGTCCTGTGCTCTCGTACTCCGGTGGCAAGTCCGATGTTAACATGATTAACGTGTATGATCATCTTCCATTTGATGATCCAG
 110 A N D S R M S D T C P V L S Y S G G K S D V N M I N V Y D H L P F D D P
 437 ATGGTGGAGTTTGGAAACAAGGTTGGGACATCCAGACATCGGATCAGGAATGGGCTGGGAGAAAATTGAAAGTGTTCATTGTCCCTCACTCACATAATGATCCTGGTTG
 146 D G G V W K Q G W D I Q T S D Q E W A G R K L K V F I V P H S H N D P G W
 546 GTTAAAGACGGTGGAAAGATACTTCAGCGATCAAACACAACATATTCTCAATAATATTGTGGATGCTTTGAGTCAAGACCCTGCAAGGAAGTTTATCTGGGCAGAGATG
 182 L K T V E R Y F S D Q T Q H I L N N I V D A L S Q D P A R K F I W A E M
 655 TCGTATCTCTCAATGTGGTGGGACATTGCCACACCTGATCGTAAGCAGAAAATGCAGACACTCGTGAAGAATGGACAGCTTGAGATAGTTACGGGTGGTTGGGTCATGA
 219 S Y L S M W W D I A T P D R K Q K M Q T L V K N G Q L E I V T G G W V M
 764 ATGATGAAGCAAACACTCATTACTTTGCTATGATTGATCAACTCATTGAAGGTATGGAATGGTTGAGGCGAACATTGAATGTTGTTCCAAAAAGTGGGTGGGCGATTGA
 255 N D E A N T H Y F A M I D Q L I E G M E W L R R T L N V V P K S G W A I D
 873 TCCCTTTGGTCACACCCCCACCATGGCTTATATACTGAAACAGATGAAGTTCAAAAACATGCTGATACAAAGAGTCCATTATGCAGTGAAGAAGTATCTTGCTCAGGAA
 291 P F G H T P T M A Y I L K Q M K F K N M L I Q R V H Y A V K K Y L A Q E
 982 AAGTCTCTGGAATTCAGATGGAGACAAATGTGGGATTCAGCTTCAAGTACAGACATGATGTGTCATCTCATGCCTTTCTATTCATATGATGTTCCTCATACTTGTGGCC
 328 K S L E F R W R Q M W D S A S S T D M M C H L M P F Y S Y D V P H T C G
1091 CAGACCCCAAGATTTGCTGCCAGTTTGATTTTGCTCGCTTACCCGGCGGCAAGATAACCTGCCCATGGAAAGTTCCTCCTGTTGCCATCACTGACTCCAATGTAGAAAC
 364 P D P K I C C Q F D F A R L P G G K I T C P W K V P P V A I T D S N V E T
1200 ACGAGCCGGAATACTACTTGACCAATATAGAAAAAAGTCAAAACTCTTCAAAAGTGACACCCTGCTTATTATATTAGGAGATGATTTTCGTTATTCGCTGAGCAAGGAA
 400 R A G I L L D Q Y R K K S K L F K S D T L L I I L G D D F R Y S L S K E
1309 ACCAACGATCAGTTTGACAACTACGCTCGAATTATCTCGTATGTGAATTCGCACCCAGAGTTAAACGCAAAACTTCAGTTTGGAACATTATCCGAATATTTTGATGCCA
 437 T N D Q F D N Y A R I I S Y V N S H P E L N A K L Q F G T L S E Y F D A
1418 TGAAATCTGAAGTGGGGGGAGAGGAAAAACTCCCAGCTTAAGTGGTGATTTCTTCACTTATGCTGATAGAGAAGATCACTATTGGAGTGGTTACTACACTTCACGGCC
 473 M K S E V G G E E K L P A L S G D F F T Y A D R E D H Y W S G Y Y T S R P
1527 TTACCACAAAATGCAGGAGAGAGTCCTGGAAAGCCACCTTCGAGGAGCAGAAATGTTGTTTGCGCTCTCATGGCCCAAAATCCAGTGGACAGGACTTGGTGAAACATTT
 509 Y H K M Q E R V L E S H L R G A E M L F A L S W P K I Q W T G L G E T F
1636 TCACATGAACTTTACCCACTGCTGGTCCAAGCACGTCAAAATCTTGGTTTGTTTCAACACCACGATGGTATAACAGGCACAGCAAAGGATCATGTTGTTGTTGATTACG
 546 S H E L Y P L L V Q A R Q N L G L F Q H H D G I T G T A K D H V V V D Y
1745 GGAATAAACTCATGAAGAGTGTTATGGATGCAAAGAAGGTAATTTCATACAGTGCCCAAGTTCTGTTGCAAGAAATGATCACGTTTGATCCAAATACCATGGTACTTAA
 582 G N K L M K S V M D A K K V I S Y S A Q V L L Q E M I T F D P N T M V L N
1854 CTATGATGAGGTGTATCAAGCTCAGAACCAACAACCTGCGCCTGTGGTTGTTAAGCTACCAACGAAGAATGAAGAAGCGCGGAAAGTCGTTCTCTACAACTCTCTGGAT
 618 Y D E V Y Q A Q N Q Q P A P V V V K L P T K N E E A R K V V L Y N S L D
1963 TACGACAGAACTGGTGTCGTGCGTCTAATTGTTACGTCACCCGACGTGGTTGTGATGTCAGAAAACAAAAACGTCGTTCCATCGCAAACCAGTCCGATCTGGTCAGATT
 655 Y D R T G V V R L I V T S P D V V V M S E N K N V V P S Q T S P I W S D
2072 CGACGGAGATCCGCACAGACCAGTTTGAACTGGTTTTCCTTTCAACTGTTCCCGCGATAGGACTGGCGGTGTACAAGATATGGGAAGACAACGACGTAGCAGACACCAC
 691 S T E I R T D Q F E L V F L S T V P A I G L A V Y K I W E D N D V A D T T
2181 GCACTCAACTGTTAAGTTTATCAACCCGAGAGTTGGGTTTTCGAAACGAACCCGCAGTAAGTTTGTACTCGACGTTGAGGATAGCGGGGAGTTTACCATCATGAATGAC
 727 H S T V K F I N P R V G F S K R T R S K F V L D V E D S G E F T I M N D
2290 CAATTAGTTGCGCATTTCTCTGGACAAAACGGGATGCTGCAGTCAGTCACCACTGTGCGTGACAACGTTAAAACGCAGCTCGGAATTGAATTCGTCGCTTATACTTCTC
 764 Q L V A H F S G Q N G M L Q S V T T V R D N V K T Q L G I E F V A Y T S
2399 GTAATAAGAAAGACAAGAGCGGCGCTTACTTGTTCCTGCCTGCTGGACCAGCACAACCGCATGTAACAGAATCCCACCGACCGTTAGTAAGGATCATCAGGGGTCCAGT
 800 R N K K D K S G A Y L F L P A G P A Q P H V T E S H R P L V R I I R G P V
2508 GATGTCAACGGTGCATGTTCTACTACCGAACGTTCTGCATAAAGTTACCCTATACACCGGTACTGGTGCAGGCACGCAGTCTTTAGGCGTCCACGTCTCTAACGACGTC
 836 M S T V H V L L P N V L H K V T L Y T G T G A G T Q S L G V H V S N D V
2617 GACGTTAGAACTGGCTACGACAACAAAGAACTCAGTATGAGGTTAAACAGCGAAGTTTTATCGGGAAGCAAATTCTTTACGGATTTAAACGGTTTCCAAATTCAACCCC
 873 D V R T G Y D N K E L S M R L N S E V L S G S K F F T D L N G F Q I Q P
2726 GAACCACGTATTCTAAACTGCCACTACAAGCAAACTTCTACCCAATACCCACAATGGCGTTCATACAAGACGAAAAATCAAGATTAACTTTGATGACGGCCCAACCACT
 909 R T T Y S K L P L Q A N F Y P I P T M A F I Q D E K S R L T L M T A Q P L
2835 GGGTGTTGCCTCACTGAAGTCAGGTCAACTTGAGGTGGTTTTGGATCGCCGTTTAATGCAGGACGACAACAGCGGGGGTGGGTCAAGGTGTGAAAGATAATTTACCAACT
 945 G V A S L K S G Q L E V V L D R R L M Q D D N R G V G Q G V K D N L P T
2944 CCTGAGAGTTTCGTGATCATGCTGGAAAGATGGACCGCTATTGCAGCGAAAGAAAGCAAATCGTCAGCGAAGCTCGCGTATCCATCTATGGCTGTGTATCAGTCATCAT
 982 P E S F V I M L E R W T A I A A K E S K S S A K L A Y P S M A V Y Q S S
3053 GGGAATTGCTACACCCAATACGTCCAATGTCGGTAAATGGGCCGGTACATTTGAAAGAAGATTACCGCTCGCTGCCACAGCCTTTACCATGCGACGTGCACGTGTTAAA
1018 W E L L H P I R P M S V N G P V H L K E D Y R S L P Q P L P C D V H V L N
3162 CTTGCGAGCAATTCATTCTAAAGATGCAGTTGCCCCTACCGACCAATCGGCTCTGCTTCTACACACAGTTGGGCGCGAATGCTCCTTGGACGCGGATAAGTATTTCCAC
1054 L R A I H S K D A V A P T D Q S A L L L H T V G R E C S L D A D K Y F H
3271 CCAACGTGCCTCATGCACGGCGTCGAGAAATTGGCTATCACGATCTCGACGCTTTTTACTAACTCTGGCATGCGGAAGACGTCGCTGTCCTTACAACACGACGGCTCGT
1091 P T C L M H G V E K L A I T I S T L F T N S G M R K T S L S L Q H D G S
3380 TGCTGGACAACCAAGGCGGTATTACAGTTTCCCCAATGGAGATACAAGCTTACAAAATAGTACTGACGTAA
1127 L L D N Q G G I T V S P M E I Q A Y K I V L T
```

FIG. 28

Drosophila mannosidase II (X77652)

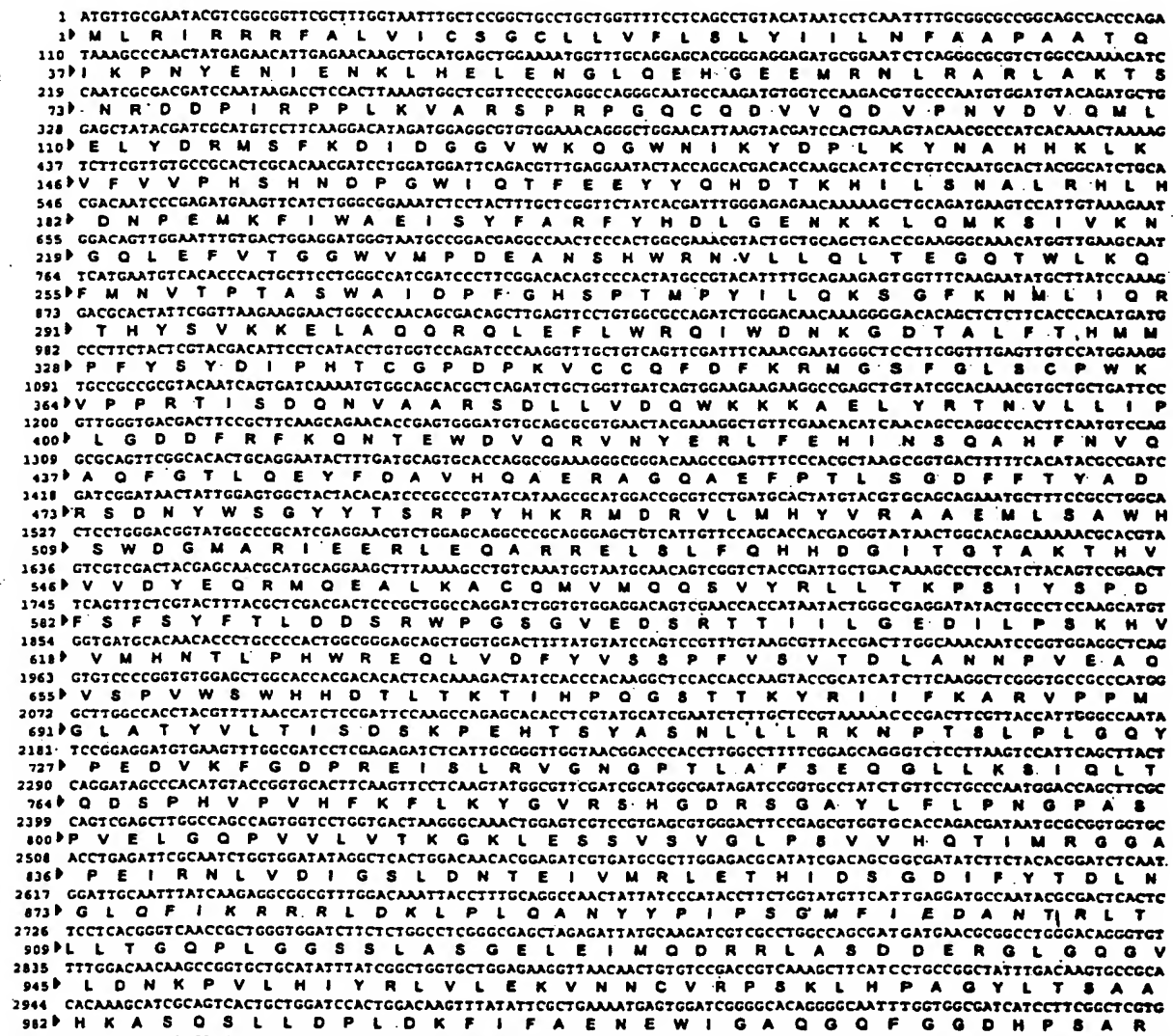

FIG. 29

Human mannosidase II (U31520)

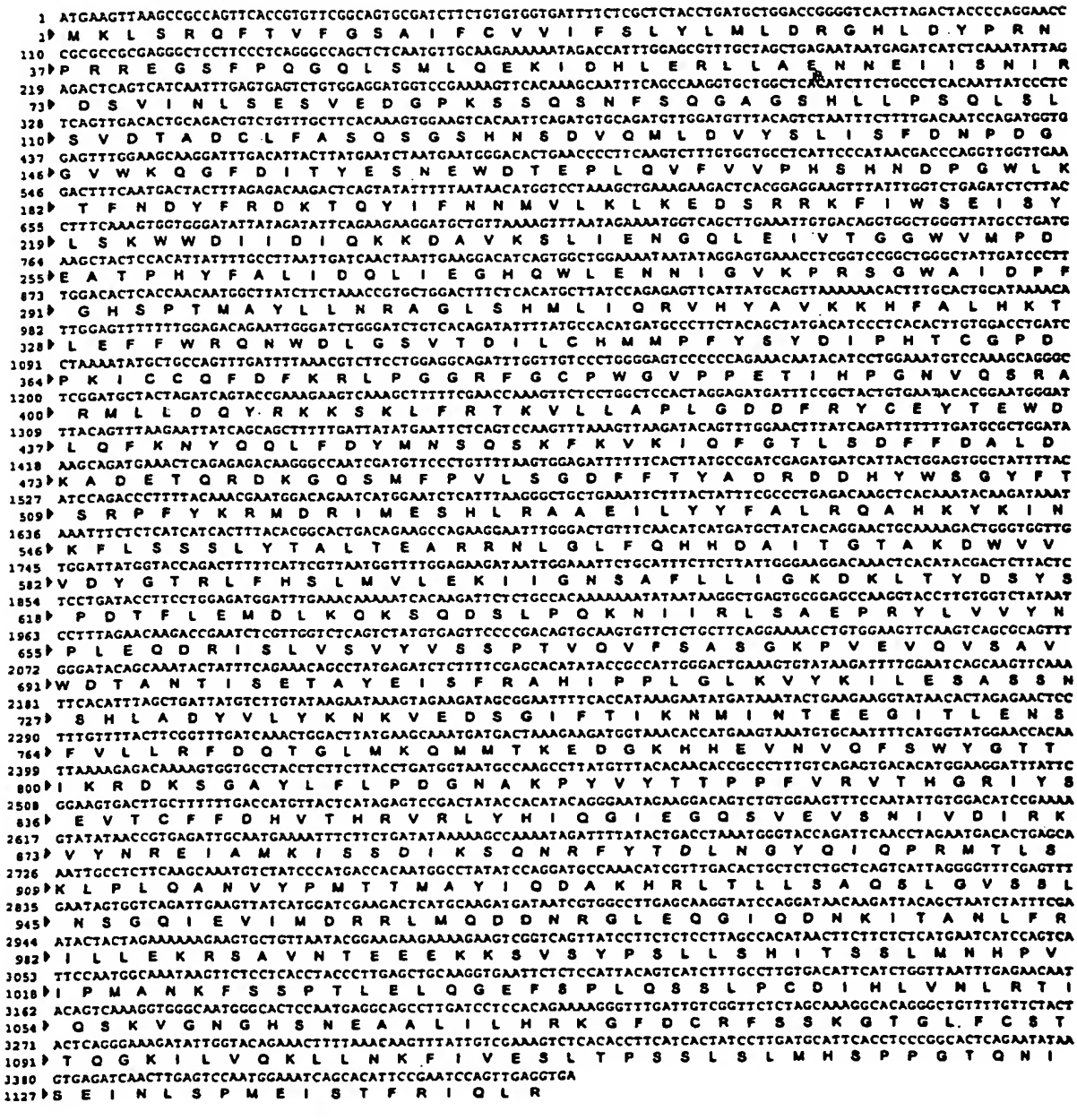

FIG. 30

Mouse mannosidase II (X61172)

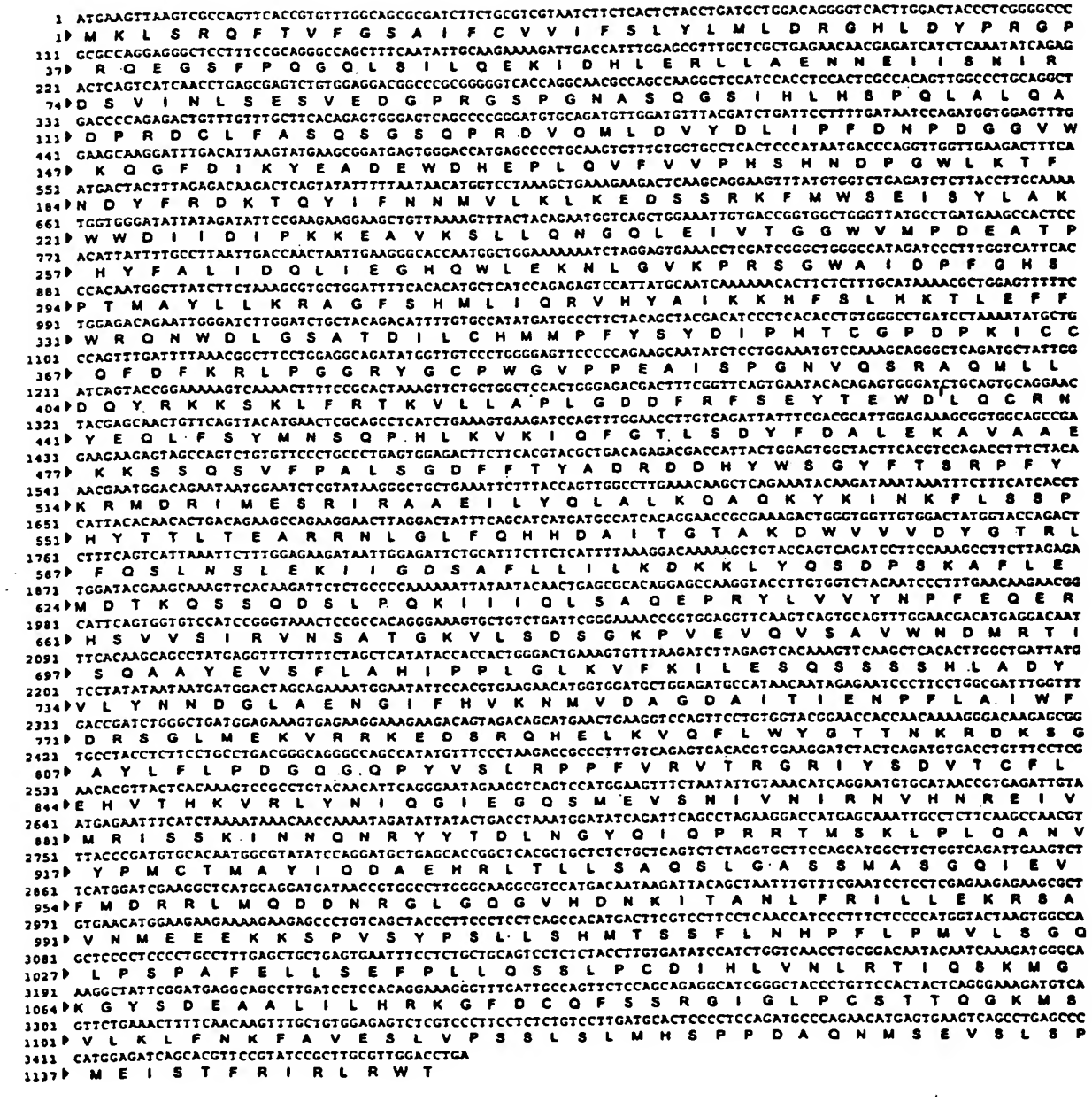

FIG. 31

Rat mannosidase II (XM_218816)

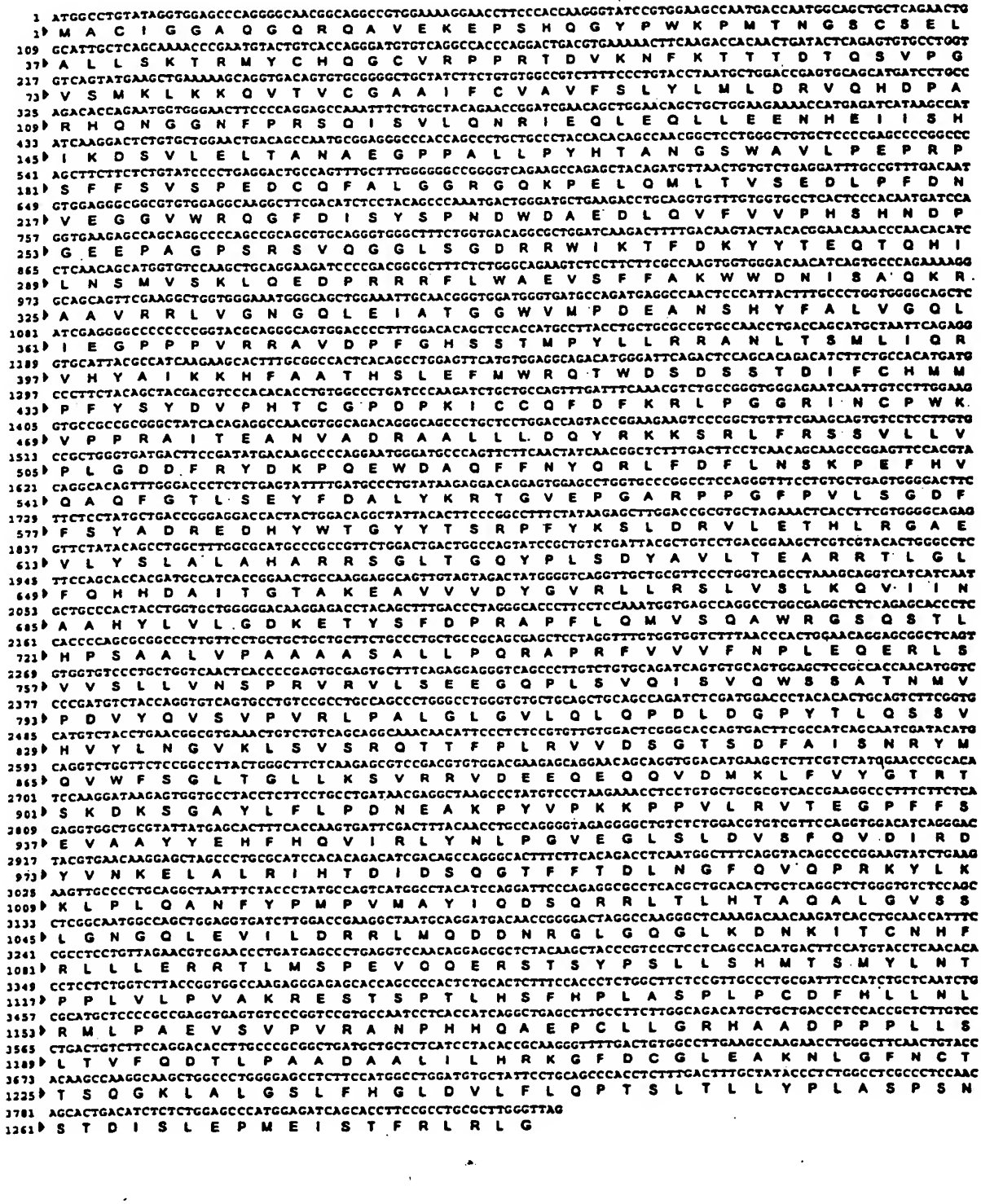

FIG. 32

Human mannosidase IIx (D55649)

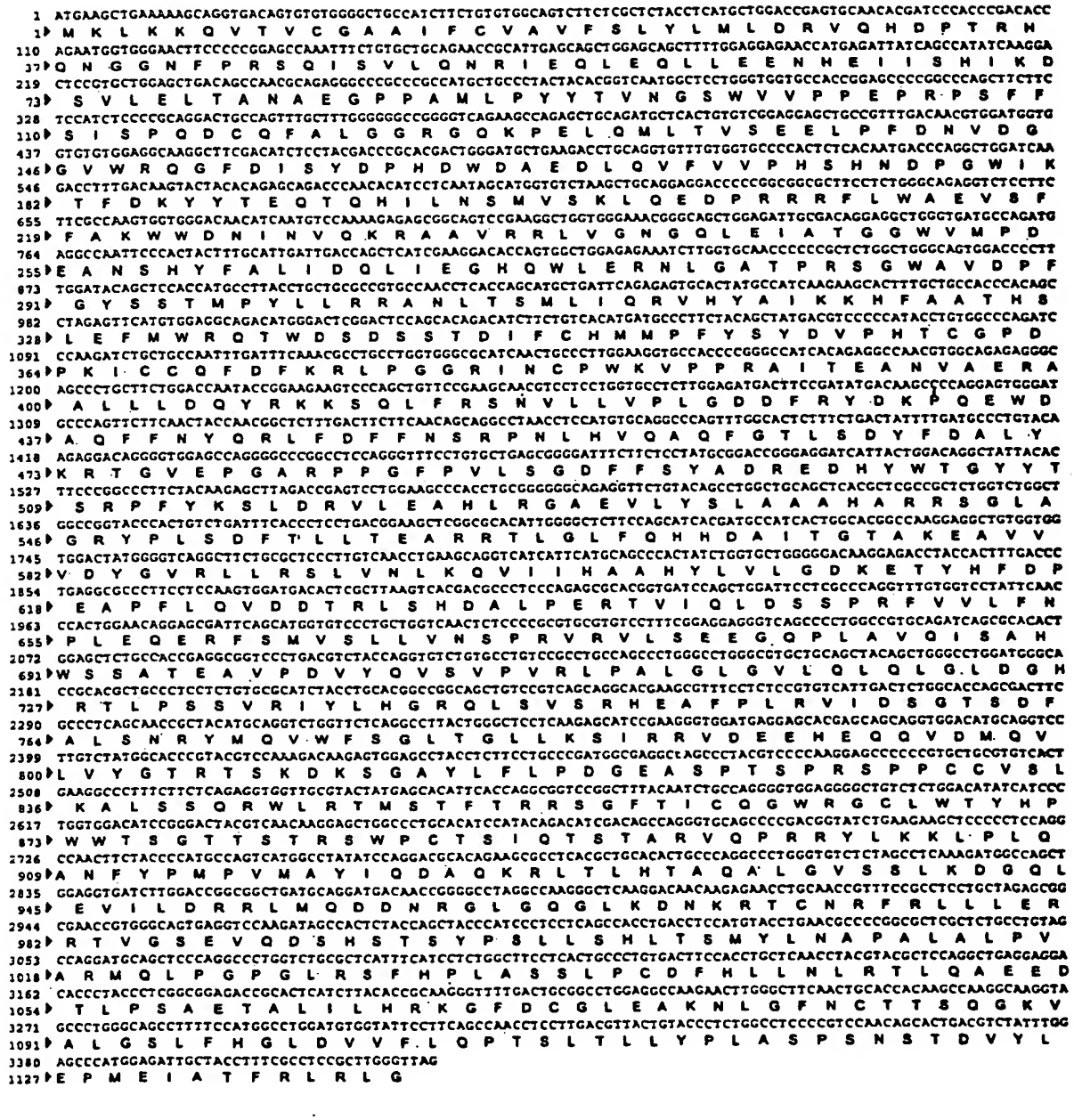

FIG. 33

Insect cell mannosidase III (AF005034)

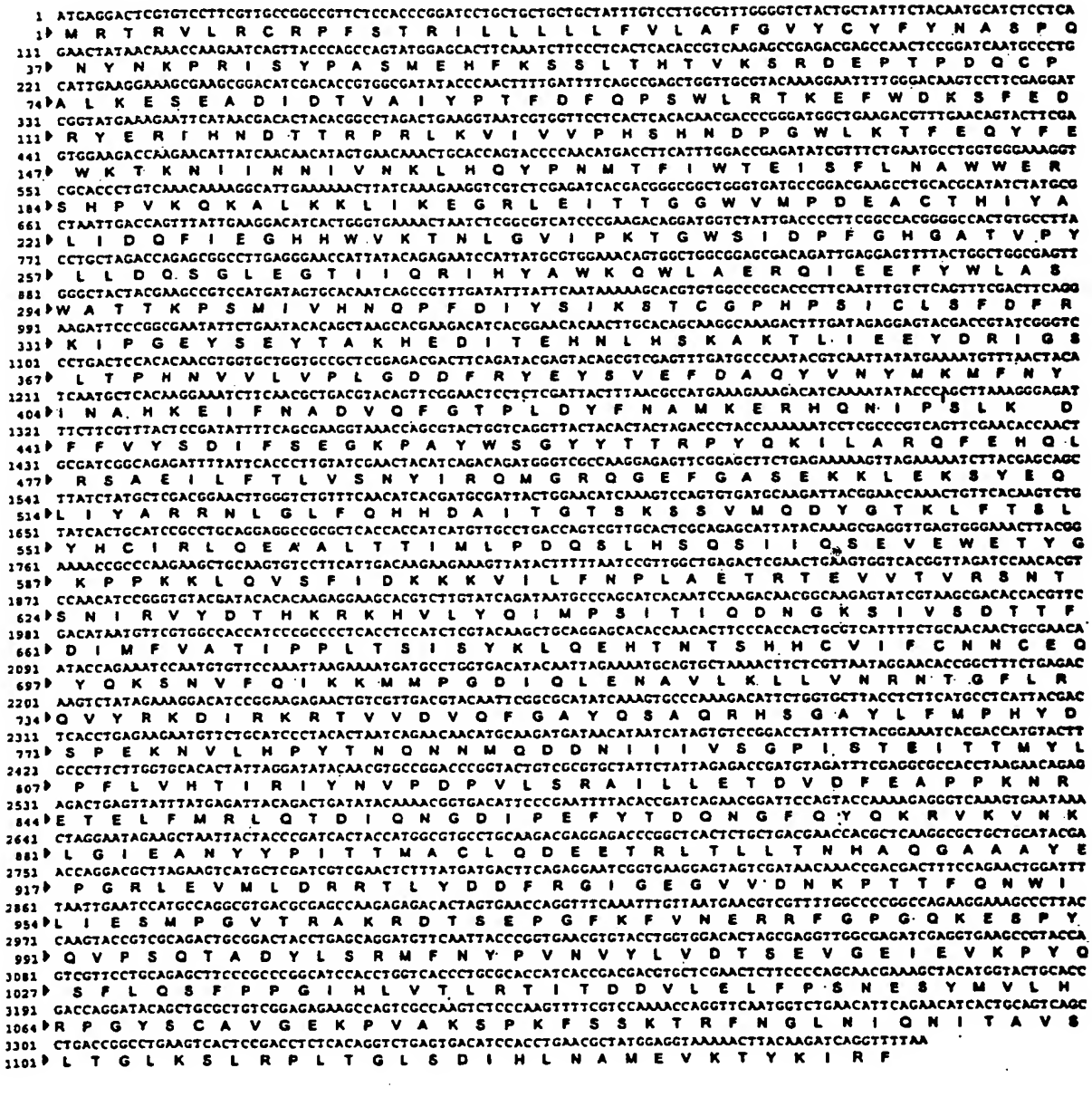

FIG. 34

Human lysosomal mannosidase II (NM_000528)

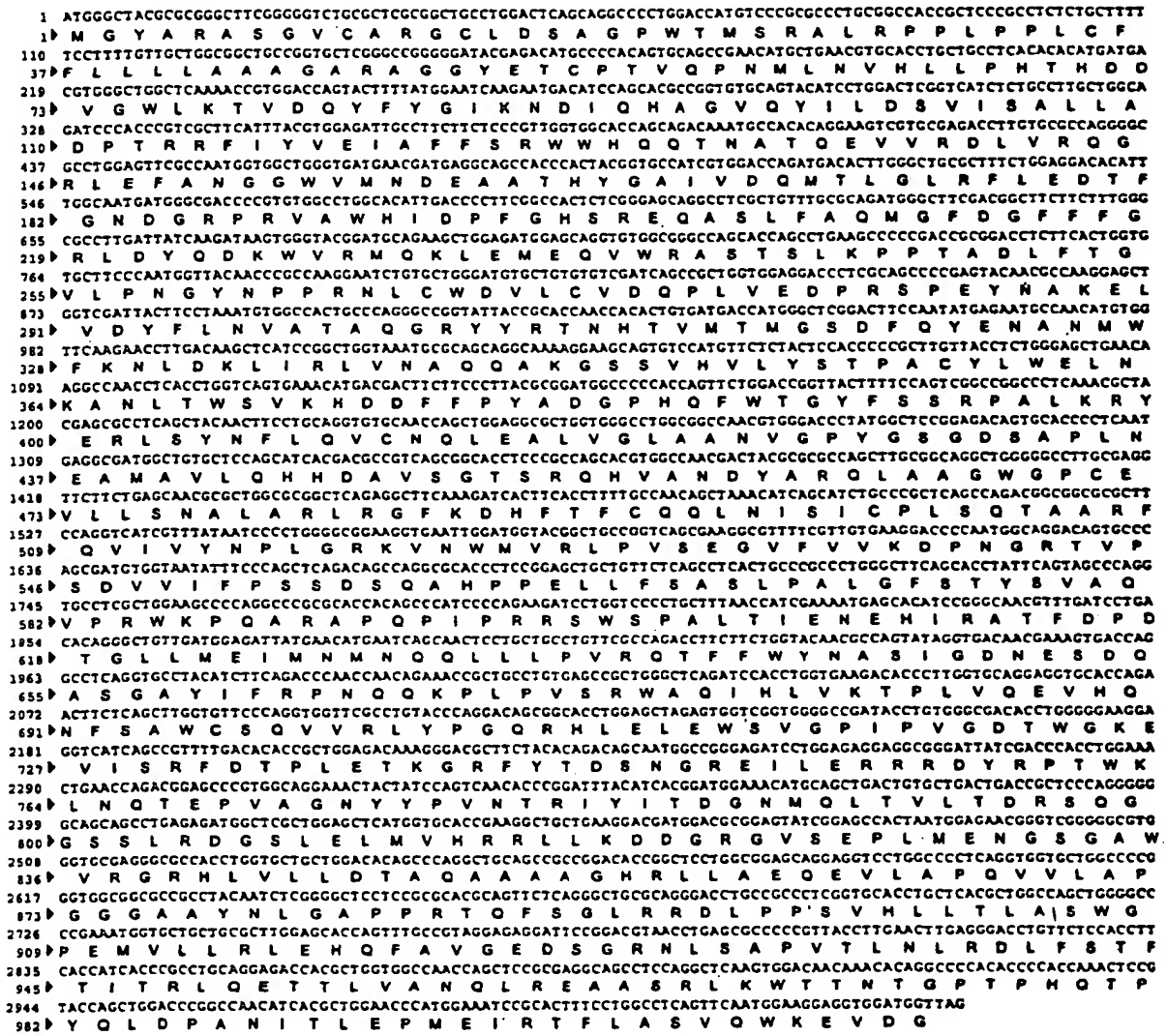

FIG. 35

Human cytoplasmic mannosidase II (NM_006715)

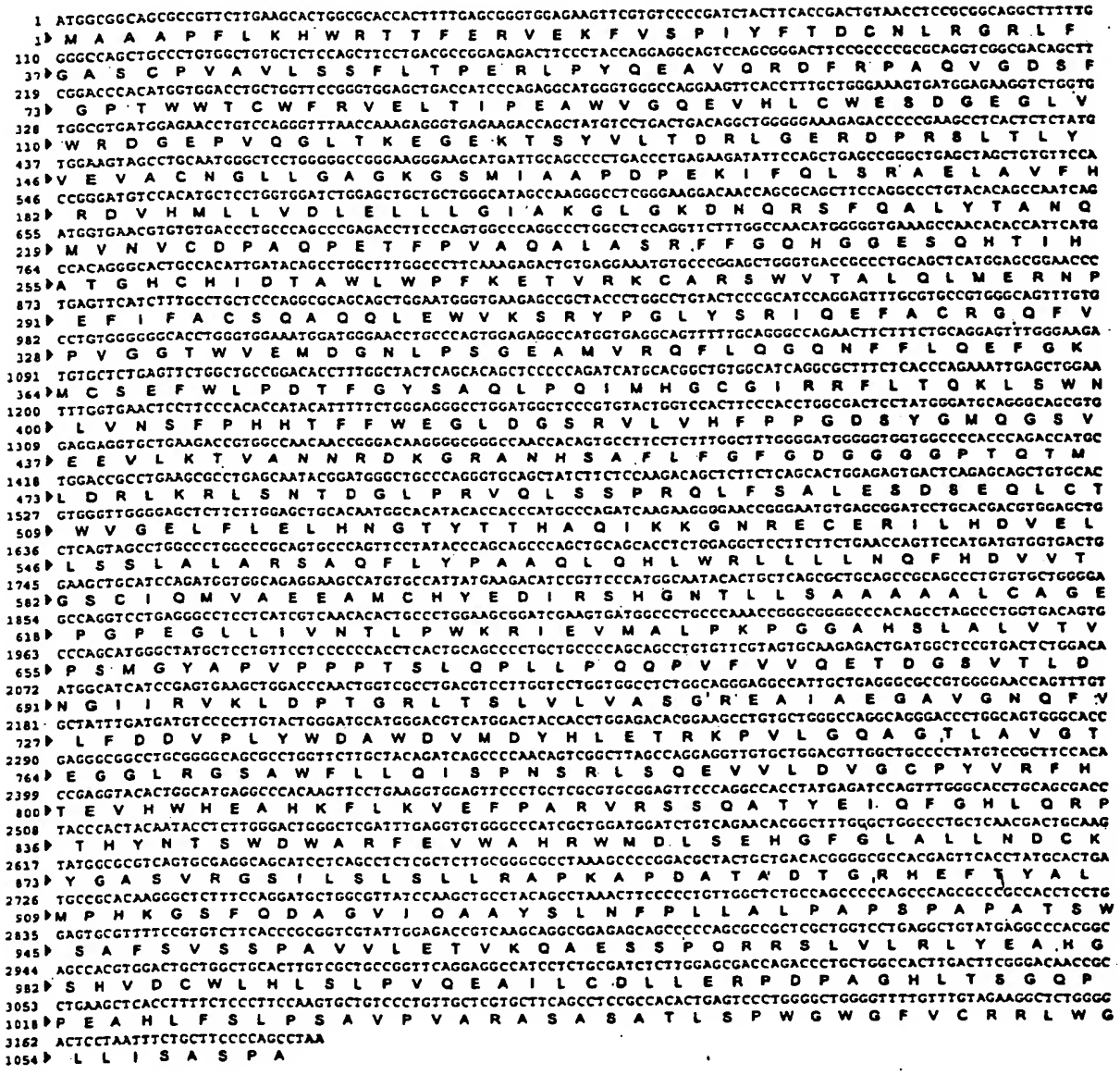

Figure 36A

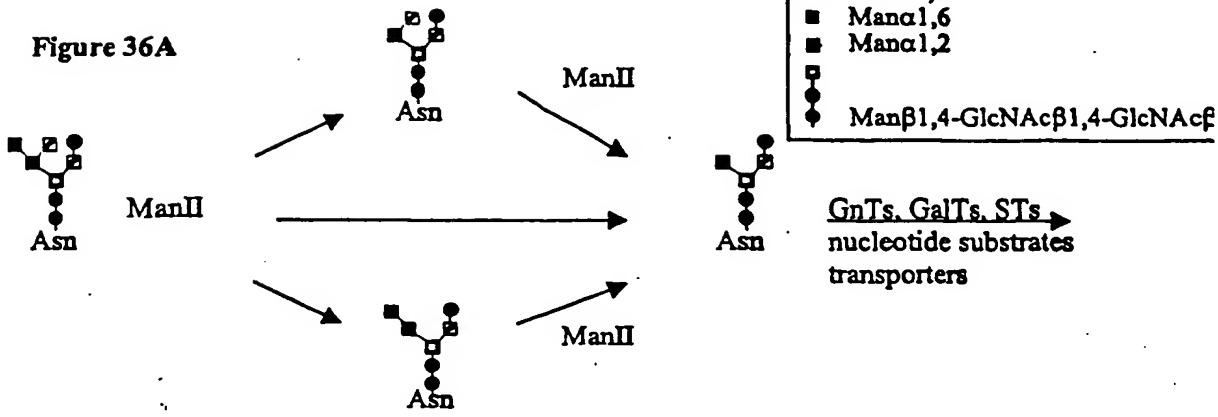

Figure 36B

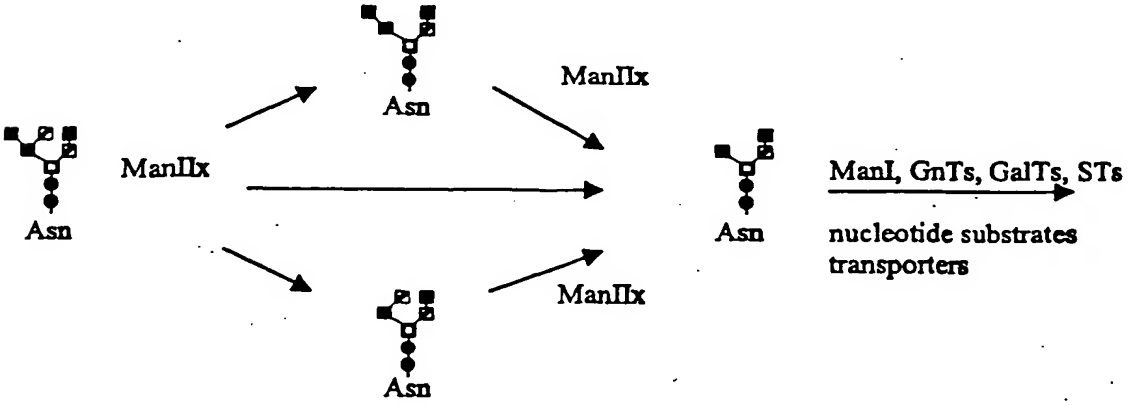

Figure 36C